

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 08:15:07 ; Search time 36 Seconds
(without alignments)
70.327 Million cell updates/sec

Title: US-09-687-993-18

Perfect score: 104

Sequence: 1 NPENSRGKGRGQKMRG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	104	100.0	19	AAW15722	Truncated GDNF N-t
2	104	100.0	20	AAW15723	Truncated GDNF N-t
3	104	100.0	21	AAW15724	Truncated GDNF N-t
4	104	100.0	22	AAW15725	Truncated GDNF N-t
5	104	100.0	23	AAW15726	Truncated GDNF N-t
6	104	100.0	24	AAW15727	Truncated GDNF N-t
7	104	100.0	25	AAW15728	Truncated GDNF N-t
8	104	100.0	26	AAW15729	Truncated GDNF N-t
9	104	100.0	27	AAW15730	Truncated GDNF N-t
10	104	100.0	28	AAW15731	Truncated GDNF N-t

11	104	100.0	29	AAW15732	Truncated GDNF N-t
12	104	100.0	30	AAW15733	Truncated GDNF N-t
13	104	100.0	31	AAW15734	Truncated GDNF N-t
14	104	100.0	32	AAW15735	Truncated GDNF N-t
15	104	100.0	33	AAW15736	Truncated GDNF N-t
16	104	100.0	34	AAW15737	Truncated GDNF N-t
17	104	100.0	35	AAW15738	Truncated GDNF N-t
18	104	100.0	36	AAW15739	Truncated GDNF N-t
19	104	100.0	37	AAW15740	Truncated GDNF N-t
20	104	100.0	38	AAW15741	Truncated GDNF N-t
21	104	100.0	39	AAW15742	Truncated GDNF N-t
22	104	100.0	133	AAW15736	Human ATF-2, Homo
23	104	100.0	133	AAW30069	Human glial-derive
24	104	100.0	134	AAW32106	Human partial glia
25	104	100.0	134	AAW18052	Mature human glial
26	104	100.0	134	AAW18058	Mature human glial
27	104	100.0	134	AAW22027	Glial cell derived
28	104	100.0	134	AAW23782	Human mature glial
29	104	100.0	134	AAW15706	Glial cell line-de
30	104	100.0	134	AAW16658	W09914235 Seq ID N
31	104	100.0	134	AAW35941	GDNF amino acid se
32	104	100.0	134	AAW51947	Human TGPbeta prot
33	104	100.0	135	AAW14930	Human glial cell l
34	104	100.0	135	AAW31945	Human glial cell l
35	104	100.0	159	AAW50698	Human GDNF protein
36	104	100.0	160	AAW38298	Human glial derive
37	104	100.0	185	AAW79375	Human ATF-1, Homo
38	104	100.0	185	AAW50697	Human GDNF protein
39	104	100.0	211	AAW83964	Human glial cell l
40	104	100.0	211	AAW50695	Human GDNF protein
41	104	100.0	211	AAW50696	Human GDNF protein
42	99	95.2	134	AAW16659	W09914235 Seq ID N
43	99	95.2	134	AAW16660	W09914235 Seq ID N
44	99	95.2	134	AAU03952	Rat GDNF polypepti
45	99	95.2	147	AAU04452	Rat mutant G-hf-GD

ALIGNMENTS

RESULT 1
AAW15722
ID AAW15722 standard; Peptide; 19 AA.
XX
AC AAW15722;
XX
DF 28-NOV-1997 (first entry)
XX
DE Truncated GDNF N-terminal peptide.
XX
KW Glial cell line-derived neurotrophic factor; GDNF; human;
KW dopaminergic; nerve cell; Parkinson's disease; gene therapy.
XX
OS Synthetic.
XX
PN W09711964-A1.
XX
PD 03-APR-1997.
XX
PF 16-SEP-1996; 96WO-US14915.
XX
PR 28-SEP-1995; 95US-0535681.
XX
PA (ANGE-) AMGEN INC.
XX
PI Hu SS;
XX
DR WPI; 1997-212849/19.
XX
PT Truncated glial cell line-derived neurotrophic factor protein - used
PT in the treatment and gene therapy of Parkinson's disease
XX
PS Claim 1; Page 83; 105pp; English.

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPENSRGKRRGGRGKNGR 19
 |||||
 DB 3 NPENSRGKRRGGRGKNGR 21

RESULT 4
 AAW15725
 ID AAW15725 standard; Peptide: 22 AA.
 XX
 AC AAW15725;
 XX
 DT 28-NOV-1997 (first entry)
 XX
 DE Truncated GDNF N-terminal peptide.
 XX
 KW Glial cell line-derived neurotrophic factor; GDNF; human;
 dopaminergic; nerve cell; Parkinson's disease; gene therapy.
 US Synthetic.
 XX
 PN WO9711964-A1.
 XX
 DT 28-NOV-1997 (first entry)
 XX
 DE Truncated GDNF N-terminal peptide.
 XX
 KW Glial cell line-derived neurotrophic factor; GDNF; human;
 dopaminergic; nerve cell; Parkinson's disease; gene therapy.
 US Synthetic.
 XX
 PN WO9711964-A1.
 XX
 DT 03-APR-1997.
 XX
 PF 16-SEP-1996; 96WO-US14915.
 XX
 PR 28-SEP-1995; 95US-0535681.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Hu SS;
 XX
 DR WPI; 1997-212849/19.
 XX
 PT Truncated glial cell line-derived neurotrophic factor protein - used
 PT in the treatment and gene therapy of Parkinson's disease
 XX
 PS Claim 1; Page 84; 105pp; English.
 XX
 CC This peptide sequence comprises amino acid residues 19-40 of the
 CC human glial cell line-derived neurotrophic factor (GDNF) protein
 CC (see AAW15706) and represents an N-terminal sequence of a novel
 CC truncated GDNF. Claimed truncated GDNF proteins have the formula:
 CC X-(Cys41-Cys133)-Y, where (Cys41-Cys133) = Cys41 through Cys133 of
 CC mature human GDNF; Y = a C-terminal Cys133 or Ile134; and X = a
 CC methionylated or nonmethionylated amine group of Cys41 or an
 CC N-terminus selected from G, RG, NRG or the N-terminal peptides
 CC given in AAW15707-42, and additions, substitutions and internal
 CC deletion variants of these. Also claimed are: a polynucleotide
 CC (see AAT60542-46) encoding a truncated GDNF (see AAW15743-45); a vector;
 CC a transformed or transfected prokaryotic or eukaryotic host cell;
 CC and a GDNF composition comprising mature GDNF protein (44 kDa) and
 CC one or more truncated GDNFs (29-40 kDa). The truncated GDNF is used
 CC in the treatment of nervous system damage caused by disease or
 CC injury, especially in the treatment of Parkinson's disease.
 XX
 SQ Sequence 22 AA;

Query Match 100.0%; Score 104; DB 18; Length 22;
 Best Local Similarity 100.0%; Pred. No. 6.5e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPENSRGKRRGGRGKNGR 19
 |||||
 DB 4 NPENSRGKRRGGRGKNGR 22

RESULT 5
 AAW15726
 ID AAW15726 standard; Peptide: 23 AA.
 XX

AC AAW15725;
 XX
 DT 28-NOV-1997 (first entry)
 XX
 DE Truncated GDNF N-terminal peptide.
 XX
 KW Glial cell line-derived neurotrophic factor; GDNF; human;
 KW dopaminergic; nerve cell; Parkinson's disease; gene therapy.
 XX
 OS Synthetic.
 XX
 PN WO9711964-A1.
 XX
 DT 03-APR-1997.
 XX
 DE 16-SEP-1996; 96WO-US14915.
 XX
 PR 28-SEP-1995; 95US-0535681.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Hu SS;
 XX
 DR WPI; 1997-212849/19.
 XX
 PT Truncated glial cell line-derived neurotrophic factor protein - used
 PT in the treatment and gene therapy of Parkinson's disease
 XX
 PS Claim 1; Page 84; 105pp; English.
 XX
 CC This peptide sequence comprises amino acid residues 18-40 of the
 CC human glial cell line-derived neurotrophic factor (GDNF) protein
 CC (see AAW15706) and represents an N-terminal sequence of a novel
 CC truncated GDNF. Claimed truncated GDNF proteins have the formula:
 CC X-(Cys41-Cys133)-Y, where (Cys41-Cys133) = Cys41 through Cys133 of
 CC mature human GDNF; Y = a C-terminal Cys133 or Ile134; and X = a
 CC methionylated or nonmethionylated amine group of Cys41 or an
 CC N-terminus selected from G, RG, NRG or the N-terminal peptides
 CC given in AAW15707-42, and additions, substitutions and internal
 CC deletion variants of these. Also claimed are: a polynucleotide
 CC (see AAT60542-46) encoding a truncated GDNF (see AAW15743-45); a vector;
 CC a transformed or transfected prokaryotic or eukaryotic host cell;
 CC and a GDNF composition comprising mature GDNF protein (44 kDa) and
 CC one or more truncated GDNFs (29-40 kDa). The truncated GDNF is used
 CC in the treatment of nervous system damage caused by disease or
 CC injury, especially in the treatment of Parkinson's disease.
 XX
 SQ Sequence 23 AA;

Query Match 100.0%; Score 104; DB 18; Length 23;
 Best Local Similarity 100.0%; Pred. No. 6.8e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPENSRGKRRGGRGKNGR 19
 |||||
 DB 5 NPENSRGKRRGGRGKNGR 23

RESULT 6
 AAW15727
 ID AAW15727 standard; Peptide: 24 AA.
 XX
 AC AAW15727;
 XX
 DT 28-NOV-1997 (first entry)
 XX
 DE Truncated GDNF N-terminal peptide.
 XX
 KW Glial cell line-derived neurotrophic factor; GDNF; human;
 KW dopaminergic; nerve cell; Parkinson's disease; gene therapy.
 XX
 OS Synthetic.
 XX

CC truncated GDNF. Claimed truncated GDNF proteins have the formula:
 CC X-(Cys41-Cys133)-Y, where (Cys41-Cys133) = Cys41 through Cys133 of
 CC mature human GDNF; Y = a C-terminal Cys133 or Ile134; and X = a
 CC methionylated or nonmethionylated amine group of Cys41 or an
 CC N-terminus selected from G, RG, NRG or the N-terminal peptides
 CC given in AAW15707-42, and additions, substitutions and internal
 CC deletion variants of these. Also claimed are: a polynucleotide
 CC (see AAT60542-46) encoding a truncated GDNF (see AAW15743-45); a vector;
 CC a transformed or transfected prokaryotic or eukaryotic host cell;
 CC and a GDNF composition comprising mature GDNF protein (44 kDa) and
 CC one or more truncated GDNFs (29-40 kDa). The truncated GDNF is used
 CC in the treatment of nervous system damage caused by disease or
 CC injury, especially in the treatment of Parkinson's disease.
 XX
 SQ Sequence 26 AA;

Query Match 100.0%; Score 104; DB 18; Length 26;
 Best Local Similarity 100.0%; Pred. No. 7.6e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NPENSRGKGRGGRGKNGR 19
 |||||
 DB 8 NPENSRGKGRGGRGKNGR 26

RESULT 9
 AAW15730
 ID AAW15730 standard; Peptide; 27 AA.

XX AAW15730;
 AC AAW15730;
 XX 28-NOV-1997 (first entry)
 DT
 DE Truncated GDNF N-terminal peptide.

XX Glial cell line-derived neurotrophic factor; GDNF; human;
 KW dopaminergic; nerve cell; Parkinson's disease; gene therapy.
 XX Synthetic.
 OS

XX WO9711964-A1.
 XX 03-APR-1997.
 PD
 PF 16-SEP-1996; 96WO-US14915.
 XX 28-SEP-1995; 95US-0535681.

PA (AMGE-) AMGEN INC.

XX Hu SS;

XX WPI; 1997-212849/19.

XX Truncated glial cell line-derived neurotrophic factor protein - used
 PT in the treatment and gene therapy of Parkinson's disease

XX Claim 1; Page 84; 105pp; English.

XX This peptide sequence comprises amino acid residues 14-40 of the
 CC human glial cell line-derived neurotrophic factor (GDNF) protein
 CC (see AAW15706) and represents an N-terminal sequence of a novel
 CC truncated GDNF. Claimed truncated GDNF proteins have the formula:
 CC X-(Cys41-Cys133)-Y, where (Cys41-Cys133) = Cys41 through Cys133 of
 CC mature human GDNF; Y = a C-terminal Cys133 or Ile134; and X = a
 CC methionylated or nonmethionylated amine group of Cys41 or an
 CC N-terminus selected from G, RG, NRG or the N-terminal peptides
 CC given in AAW15707-42, and additions, substitutions and internal
 CC deletion variants of these. Also claimed are: a polynucleotide
 CC (see AAT60542-46) encoding a truncated GDNF (see AAW15743-45); a vector;
 CC a transformed or transfected prokaryotic or eukaryotic host cell;
 CC and a GDNF composition comprising mature GDNF protein (44 kDa) and
 CC one or more truncated GDNFs (29-40 kDa). The truncated GDNF is used

CC in the treatment of nervous system damage caused by disease or
 CC injury, especially in the treatment of Parkinson's disease.
 XX
 SQ Sequence 27 AA;

Query Match 100.0%; Score 104; DB 18; Length 27;
 Best Local Similarity 100.0%; Pred. No. 7.9e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPENSRGKGRGGRGKNGR 19
 |||||
 DB 9 NPENSRGKGRGGRGKNGR 27

RESULT 10
 AAW15731
 ID AAW15731 standard; Peptide; 28 AA.

XX AAW15731;
 AC AAW15731;
 XX 28-NOV-1997 (first entry)
 DT
 DE Truncated GDNF N-terminal peptide.

XX Glial cell line-derived neurotrophic factor; GDNF; human;
 KW dopaminergic; nerve cell; Parkinson's disease; gene therapy.
 XX Synthetic.
 OS

XX WO9711964-A1.
 XX 03-APR-1997.
 PD
 PF 16-SEP-1996; 96WO-US14915.
 XX 28-SEP-1995; 95US-0535681.
 XX (AMGE-) AMGEN INC.

XX Hu SS;

XX WPI; 1997-212849/19.

XX Truncated glial cell line-derived neurotrophic factor protein - used
 PT in the treatment and gene therapy of Parkinson's disease

XX Claim 1; Page 84; 105pp; English.

XX This peptide sequence comprises amino acid residues 13-40 of the
 CC human glial cell line-derived neurotrophic factor (GDNF) protein
 CC (see AAW15706) and represents an N-terminal sequence of a novel
 CC truncated GDNF. Claimed truncated GDNF proteins have the formula:
 CC X-(Cys41-Cys133)-Y, where (Cys41-Cys133) = Cys41 through Cys133 of
 CC mature human GDNF; Y = a C-terminal Cys133 or Ile134; and X = a
 CC methionylated or nonmethionylated amine group of Cys41 or an
 CC N-terminus selected from G, RG, NRG or the N-terminal peptides
 CC given in AAW15707-42, and additions, substitutions and internal
 CC deletion variants of these. Also claimed are: a polynucleotide
 CC (see AAT60542-46) encoding a truncated GDNF (see AAW15743-45); a vector;
 CC a transformed or transfected prokaryotic or eukaryotic host cell;
 CC and a GDNF composition comprising mature GDNF protein (44 kDa) and
 CC one or more truncated GDNFs (29-40 kDa). The truncated GDNF is used
 CC in the treatment of nervous system damage caused by disease or
 CC injury, especially in the treatment of Parkinson's disease.
 XX

XX Sequence 28 AA;

Query Match 100.0%; Score 104; DB 18; Length 28;
 Best Local Similarity 100.0%; Pred. No. 8.1e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPENSRGKGRGGRGKNGR 19
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Db      10 NPENSRGKGRGGRGKNGR 28
RESULT 11
AAW15732
ID      AAW15732 standard; Peptide; 29 AA.
XX
XX      AAW15732;
AC
XX
XX      28-NOV-1997 (first entry)
DT
XX
XX      Truncated GDNF N-terminal peptide.
DE
XX
XX      Glial cell line-derived neurotrophic factor; GDNF; human;
KW      dopaminergic; nerve cell; Parkinson's disease; gene therapy.
XX
XX      Synthetic.
OS
XX
XX      WO9711964-A1.
PN
XX
XX      03-APR-1997.
PD
XX
XX      16-SEP-1996; 96WO-US14915.
PF
XX
XX      28-SEP-1995; 95US-0535681.
PR
XX
XX      (AMGE-) AMGEN INC.
PA
XX
XX      Hu SS;
PI
XX
XX      WPI; 1997-212849/19.
PD
XX
XX      Truncated glial cell line-derived neurotrophic factor protein - used
PT      in the treatment and gene therapy of Parkinson's disease
PT
XX
XX      Claim 1; Page 84; 105pp; English.
PS
XX
XX      This peptide sequence comprises amino acid residues 11-40 of the
CC      human glial cell line-derived neurotrophic factor (GDNF) protein
CC      (see AAW15706) and represents an N-terminal sequence of a novel
CC      truncated GDNF. Claimed truncated GDNF proteins have the formula:
CC      X-(Cys41-Cys133)-Y, where (Cys41-Cys133) = Cys41 through Cys133 of
CC      mature human GDNF; Y = a C-terminal Cys133 or Ile134; and X = a
CC      methionylated or nonmethionylated amine group of Cys41 or an
CC      N-terminus selected from G, RG, NRG or the N-terminal peptides
CC      given in AAW15707-42, and additions, substitutions and internal
CC      deletion variants of these. Also claimed are: a polynucleotide
CC      (see AAT60542-46) encoding a truncated GDNF (see AAW15743-45); a vector;
CC      a transformed or transfected prokaryotic or eukaryotic host cell;
CC      and a GDNF composition comprising mature GDNF protein (44 kDa) and
CC      one or more truncated GDNFs (29-40 kDa). The truncated GDNF is used
CC      in the treatment of nervous system damage caused by disease or
CC      injury, especially in the treatment of Parkinson's disease.
XX
XX      Sequence 29 AA:
SQ
XX      Query Match 100.0%; Score 104; DB 18; Length 29;
XX      Best Local Similarity 100.0%; Pred. No. 8.4e-08;
XX      Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NPENSRGKGRGGRGKNGR 19
      |||||
Db      11 NPENSRGKGRGGRGKNGR 29
RESULT 12
AAW15733
ID      AAW15733 standard; Peptide; 30 AA.
XX
XX      AAW15733;
AC
XX
XX      28-NOV-1997 (first entry)
DT
XX
XX      Truncated GDNF N-terminal peptide.
DE
XX
XX      Glial cell line-derived neurotrophic factor; GDNF; human;
KW      dopaminergic; nerve cell; Parkinson's disease; gene therapy.
XX
XX      Synthetic.
OS
XX
XX      WO9711964-A1.
PN
XX
XX      03-APR-1997.
PD
XX
XX      16-SEP-1996; 96WO-US14915.
PF
XX
XX      28-SEP-1995; 95US-0535681.
PR
XX
XX      (AMGE-) AMGEN INC.
PA
XX
XX      Hu SS;
PI
XX
XX      WPI; 1997-212849/19.
PD
XX
XX      Truncated glial cell line-derived neurotrophic factor protein - used
PT      in the treatment and gene therapy of Parkinson's disease
PT
XX
XX      Claim 1; Page 84; 105pp; English.
PS
XX
XX      This peptide sequence comprises amino acid residues 12-40 of the
CC      human glial cell line-derived neurotrophic factor (GDNF) protein
CC      (see AAW15706) and represents an N-terminal sequence of a novel
CC      truncated GDNF. Claimed truncated GDNF proteins have the formula:
CC      X-(Cys41-Cys133)-Y, where (Cys41-Cys133) = Cys41 through Cys133 of
CC      mature human GDNF; Y = a C-terminal Cys133 or Ile134; and X = a
CC      methionylated or nonmethionylated amine group of Cys41 or an
CC      N-terminus selected from G, RG, NRG or the N-terminal peptides
CC      given in AAW15707-42, and additions, substitutions and internal
CC      deletion variants of these. Also claimed are: a polynucleotide
CC      (see AAT60542-46) encoding a truncated GDNF (see AAW15743-45); a vector;
CC      a transformed or transfected prokaryotic or eukaryotic host cell;
CC      and a GDNF composition comprising mature GDNF protein (44 kDa) and
CC      one or more truncated GDNFs (29-40 kDa). The truncated GDNF is used
CC      in the treatment of nervous system damage caused by disease or
CC      injury, especially in the treatment of Parkinson's disease.
XX
XX      Sequence 30 AA:
SQ
XX      Query Match 100.0%; Score 104; DB 18; Length 30;
XX      Best Local Similarity 100.0%; Pred. No. 8.7e-08;
XX      Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NPENSRGKGRGGRGKNGR 19
      |||||
Db      12 NPENSRGKGRGGRGKNGR 30
RESULT 13
AAW15734
ID      AAW15734 standard; Peptide; 31 AA.
XX
XX      AAW15734;
AC
XX
XX      28-NOV-1997 (first entry)
DT
XX
XX      Truncated GDNF N-terminal peptide.
DE
XX
XX      Glial cell line-derived neurotrophic factor; GDNF; human;
KW      dopaminergic; nerve cell; Parkinson's disease; gene therapy.
XX
XX      Synthetic.
OS
XX
XX      WO9711964-A1.
PN
XX
XX      03-APR-1997.
PD
XX
XX      16-SEP-1996; 96WO-US14915.
PF
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XX      28-SEP-1995; 95US-0535681.
PR
XX
XX      (AMGE-) AMGEN INC.
PA
XX
XX      Hu SS;
PI
XX
XX      WPI; 1997-212849/19.
PD
XX
XX      Truncated glial cell line-derived neurotrophic factor protein - used
PT      in the treatment and gene therapy of Parkinson's disease
PT
XX
XX      Claim 1; Page 84; 105pp; English.
PS
XX
XX      This peptide sequence comprises amino acid residues 11-40 of the
CC      human glial cell line-derived neurotrophic factor (GDNF) protein
CC      (see AAW15706) and represents an N-terminal sequence of a novel
CC      truncated GDNF. Claimed truncated GDNF proteins have the formula:
CC      X-(Cys41-Cys133)-Y, where (Cys41-Cys133) = Cys41 through Cys133 of
CC      mature human GDNF; Y = a C-terminal Cys133 or Ile134; and X = a
CC      methionylated or nonmethionylated amine group of Cys41 or an
CC      N-terminus selected from G, RG, NRG or the N-terminal peptides
CC      given in AAW15707-42, and additions, substitutions and internal
CC      deletion variants of these. Also claimed are: a polynucleotide
CC      (see AAT60542-46) encoding a truncated GDNF (see AAW15743-45); a vector;
CC      a transformed or transfected prokaryotic or eukaryotic host cell;
CC      and a GDNF composition comprising mature GDNF protein (44 kDa) and
CC      one or more truncated GDNFs (29-40 kDa). The truncated GDNF is used
CC      in the treatment of nervous system damage caused by disease or
CC      injury, especially in the treatment of Parkinson's disease.
XX
XX      Sequence 31 AA:
SQ
XX      Query Match 100.0%; Score 104; DB 18; Length 31;
XX      Best Local Similarity 100.0%; Pred. No. 8.7e-08;
XX      Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NPENSRGKGRGGRGKNGR 19
      |||||
Db      13 NPENSRGKGRGGRGKNGR 31

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PF 16-SEP-1996; 96WO-US14915.
 XX
 PR 28-SEP-1995; 95US-0535681.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Hu SS;
 XX
 DR WPI; 1997-212849/19.
 XX
 PT Truncated glial cell line-derived neurotrophic factor protein - used
 PT in the treatment and gene therapy of Parkinson's disease
 XX
 PS Claim 1; Page 84; 105pp; English.
 XX
 CC This peptide sequence comprises amino acid residues 10-40 of the
 CC human glial cell line-derived neurotrophic factor (GDNF) protein
 CC (see AAW15706) and represents an N-terminal sequence of a novel
 CC truncated GDNF. Claimed truncated GDNF proteins have the formula:
 CC X-(Cys41-Cys133)-Y, where (Cys41-Cys133) = Cys41 through Cys133 of
 CC mature human GDNF; Y = a C-terminal Cys133 or Ile134; and X = a
 CC methionylated or nonmethionylated amine group of Cys41 or an
 CC N-terminus selected from G, RG, NRG or the N-terminal peptides
 CC given in AAW15707-42, and additions, substitutions and internal
 CC deletion variants of these. Also claimed are: a polynucleotide
 CC (see AAT60542-46) encoding a truncated GDNF (see AAW15743-45); a vector;
 CC a transformed or transfected prokaryotic or eukaryotic host cell;
 CC and a GDNF composition comprising mature GDNF protein (44 kDa) and
 CC one or more truncated GDNFs (29-40 kDa). The truncated GDNF is used
 CC in the treatment of nervous system damage caused by disease or
 CC injury, especially in the treatment of Parkinson's disease.
 XX
 SQ Sequence 31 AA;
 Query Match 100.0%; Score 104; DB 18; Length 31;
 Best Local Similarity 100.0%; Pred. No. 9e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NPENSRGKRGRRGQGNKRG 19
 DB 13 NPENSRGKRGRRGQGNKRG 31
 RESULT 14
 AAW15735
 ID AAW15735 standard; Peptide; 32 AA.
 XX
 AC AAW15735;
 XX
 DT 28-NOV-1997 (first entry)
 XX
 DE Truncated GDNF N-terminal peptide.
 XX
 KW Glial cell line-derived neurotrophic factor; GDNF; human;
 KW dopaminergic; nerve cell; Parkinson's disease; gene therapy.
 XX
 OS Synthetic.
 XX
 PN W09711964-A1.
 XX
 PD 03-APR-1997.
 XX
 PF 16-SEP-1996; 96WO-US14915.
 XX
 PR 28-SEP-1995; 95US-0535681.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Hu SS;
 XX
 DR WPI; 1997-212849/19.
 XX
 PT Truncated glial cell line-derived neurotrophic factor protein - used

PT in the treatment and gene therapy of Parkinson's disease
 XX
 PS Claim 1; Page 84; 105pp; English.
 XX
 CC This peptide sequence comprises amino acid residues 9-40 of the
 CC human glial cell line-derived neurotrophic factor (GDNF) protein
 CC (see AAW15706) and represents an N-terminal sequence of a novel
 CC truncated GDNF. Claimed truncated GDNF proteins have the formula:
 CC X-(Cys41-Cys133)-Y, where (Cys41-Cys133) = Cys41 through Cys133 of
 CC mature human GDNF; Y = a C-terminal Cys133 or Ile134; and X = a
 CC methionylated or nonmethionylated amine group of Cys41 or an
 CC N-terminus selected from G, RG, NRG or the N-terminal peptides
 CC given in AAW15707-42, and additions, substitutions and internal
 CC deletion variants of these. Also claimed are: a polynucleotide
 CC (see AAT60542-46) encoding a truncated GDNF (see AAW15743-45); a vector;
 CC a transformed or transfected prokaryotic or eukaryotic host cell;
 CC and a GDNF composition comprising mature GDNF protein (44 kDa) and
 CC one or more truncated GDNFs (29-40 kDa). The truncated GDNF is used
 CC in the treatment of nervous system damage caused by disease or
 CC injury, especially in the treatment of Parkinson's disease.
 XX
 SQ Sequence 32 AA;
 Query Match 100.0%; Score 104; DB 18; Length 32;
 Best Local Similarity 100.0%; Pred. No. 9.2e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NPENSRGKRGRRGQGNKRG 19
 DB 14 NPENSRGKRGRRGQGNKRG 32
 RESULT 15
 AAW15736
 ID AAW15736 standard; Peptide; 33 AA.
 XX
 AC AAW15736;
 XX
 DT 28-NOV-1997 (first entry)
 XX
 DE Truncated GDNF N-terminal peptide.
 XX
 KW Glial cell line-derived neurotrophic factor; GDNF; human;
 KW dopaminergic; nerve cell; Parkinson's disease; gene therapy.
 XX
 OS Synthetic.
 XX
 PN W09711964-A1.
 XX
 PD 03-APR-1997.
 XX
 PF 16-SEP-1996; 96WO-US14915.
 XX
 PR 28-SEP-1995; 95US-0535681.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Hu SS;
 XX
 DR WPI; 1997-212849/19.
 XX
 PT Truncated glial cell line-derived neurotrophic factor protein - used
 PT in the treatment and gene therapy of Parkinson's disease
 XX
 PS Claim 1; Page 84; 105pp; English.
 XX
 CC This peptide sequence comprises amino acid residues 8-40 of the
 CC human glial cell line-derived neurotrophic factor (GDNF) protein
 CC (see AAW15706) and represents an N-terminal sequence of a novel
 CC truncated GDNF. Claimed truncated GDNF proteins have the formula:
 CC X-(Cys41-Cys133)-Y, where (Cys41-Cys133) = Cys41 through Cys133 of
 CC mature human GDNF; Y = a C-terminal Cys133 or Ile134; and X = a
 CC methionylated or nonmethionylated amine group of Cys41 or an

CC N-terminus selected from G, RG, NRG or the N-terminal peptides
CC given in AAW15707-42, and additions, substitutions and internal
CC deletion variants of these. Also claimed are: a polynucleotide
CC (see AAT60542-46) encoding a truncated GDNF (see AAW15743-45); a vector;
CC a transfected or transcribed prokaryotic or eukaryotic host cell;
CC and a GDNF composition comprising mature GDNF protein (44 kDa) and
CC one or more truncated GDNFs (29-40 kDa). The truncated GDNF is used
CC in the treatment of nervous system damage caused by disease or
CC injury, especially in the treatment of Parkinson's disease.
XX
SQ Sequence 33 AA;

Query Match 100.0%; Score 104; DB 18; Length 33;
Best Local Similarity 100.0%; Pred. No. 9.5e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPENSRGKRRGQGGKNRG 19
DB 15 NPENSRGKRRGQGGKNRG 33

rch completed: December 4, 2002, 08:17:58
time : 37 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 08:17:02 ; Search time 16 Seconds
(without alignments)
114.160 Million cell updates/sec

Title: US-09-687-993-18

Perfect score: 104

Sequence: 1 NPENSRGKRRGQKNG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

al number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	104	100.0	211	2 B37499	glial cell line-de
2	99	95.2	211	2 A37499	glial cell line-de
3	99	95.2	211	2 I49686	glial cell line-de
4	55.5	53.4	2925	2 T00133	RNA-directed RNA p
5	54	51.9	898	2 H87481	ribonuclease, Rne/
6	51	49.0	525	2 B48058	RNA-binding protei
7	51	49.0	750	2 A97501	topoisomerase iv c
8	51	49.0	750	2 AE2719	topoisomerase IV s
9	51	49.0	1334	2 E86451	probable copia-ty
10	50	48.1	340	1 WMBEL1	latency-related pr
11	50	48.1	613	2 F64056	probable ATP-depen
12	49.5	47.6	236	2 T01458	hypothetical prote
13	49.5	47.6	893	2 AH1867	hypothetical prote
14	49	47.1	165	2 T39586	RNA binding protei
15	49	47.1	434	2 S36341	E2 protein - human
16	48.5	46.6	637	2 G88533	70.5K hypothetical
17	48.5	46.6	633	2 T02673	heterogeneous nucl
18	48	46.2	126	2 T16952	hypothetical prote
19	47.5	45.7	117	2 T38440	small nuclear ribo
20	47.5	45.7	523	2 E96576	unknown protein, 4
21	47.5	45.7	695	2 I51552	dsRNA-binding prot
22	47.5	45.7	1339	2 T47841	hypothetical prote
23	47	45.2	269	2 JCT7700	38K ribosome-assoc
24	47	45.2	300	2 T49225	hypothetical prote
25	47	45.2	536	2 T42606	probable transcrip
26	47	45.2	656	2 D96831	hypothetical prote
27	47	45.2	849	2 A96592	hypothetical prote
28	47	45.2	1171	2 T05039	hypothetical prote
29	46.5	44.7	800	2 I51653	dsRNA-binding prot

30	46.5	44.7	1188	2 D86311	protein Flt3.20 (1
31	46	44.2	65	2 D71352	hypothetical prote
32	46	44.2	243	2 A96744	hypothetical prote
33	46	44.2	321	2 A38712	fibillarlin (valid
34	46	44.2	335	2 T31600	hypothetical prote
35	46	44.2	370	2 T12180	probable transcrip
36	46	44.2	375	2 T08134	oleosin-like prote
37	46	44.2	455	2 C90738	probable ATP-depen
38	46	44.2	455	2 D85588	probable ATP-depen
39	46	44.2	551	2 S56283	protein-tyrosine-p
40	46	44.2	632	1 A40724	fragile X mental r
41	45.5	43.8	123	2 T16234	hypothetical prote
42	45.5	43.8	467	2 G86461	probable gag-poi p
43	45.5	43.8	538	2 H86335	T20H2.2 protein -
44	45	43.3	178	1 MNXR12	nonstructural prot
45	45	43.3	253	2 T41418	40S ribosomal prot

ALIGNMENTS

RESULT 1

B37499

glial cell line-derived neurotrophic factor precursor - human

N:Alternate names: GDNF

C:Species: Homo sapiens (man)

C>Date: 26-Aug-1999 #sequence_revision 26-Aug-1999 #text_change 26-Aug-1999

C:Accession: B37499

R:Lin, L.F.; Doherty, D.H.; Lille, J.D.; Bektesh, S.; Collins, F.

Science 260, 1130-1132, 1993

A:Title: GDNF: a glial cell line-derived neurotrophic factor for midbrain dopaminergi

A:Reference number: A37499; MUID:93262463; PMID:8493557

A:Accession: B37499

A:Molecule type: DNA

A:Residues: 1-211 <LIN>

A:Cross-references: GB:L15306; GB:L15306; MID:g306761; PIDN:AAA67910.1; PID:g306763

A:Note: sequence extracted from NCBI backbone (NCBIP:132084)

C:Keywords: glycoprotein; homodimer

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-77/Domain: propeptide #status predicted <PRO>

F:78-211/Product: glial cell line-derived neurotrophic factor #status predicted <MAT>

F:126,162/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 104; DB 2; Length 211;

Best Local Similarity 100.0%; Pred. No. 1.7e-07;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPENSRGKRRGQKNG 19

|||||

DB 99 NPENSRGKRRGQKNG 117

RESULT 2

A37499

glial cell line-derived neurotrophic factor precursor - rat

N:Alternate names: GDNF

N:Contains: glial cell line-derived neurotrophic factor splice form GDNF555; glial ce

C:Species: Rattus norvegicus (Norway rat)

C>Date: 16-Feb-1994 #sequence_revision 16-Feb-1994 #text_change 05-Nov-1999

C:Accession: A37499; I57605; I53427; I58180; S61537

R:Lin, L.F.; Doherty, D.H.; Lille, J.D.; Bektesh, S.; Collins, F.

Science 260, 1130-1132, 1993

A:Title: GDNF: a glial cell line-derived neurotrophic factor for midbrain dopaminergi

A:Reference number: A37499; MUID:93262463; PMID:8493557

A:Accession: A37499

A:Molecule type: mRNA; protein

A:Residues: 1-211 <LIN>

A:Cross-references: GB:L15305; MID:g310123; PIDN:AAA67909.1; PID:g310124

A:Experimental source: glial cell line B49

A:Note: sequence extracted from NCBI backbone (NCBIP:132083)

R:Springer, J.E.; Seeburger, J.L.; He, J.; Gabrea, A.; Blankenhorn, E.P.; Bergman, L.

Exp. Neurol. 131, 47-52, 1995

A:Title: cDNA sequence and differential mRNA regulation of two forms of glial cell li

RESULT 4

T00133
RNA-directed RNA polymerase (EC 2.7.7.48) - rice grassy stunt virus
C:Species: rice grassy stunt virus
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jul-2000
C:Accession: T00133
R:Toriyama, S.; Kimishima, T.; Takahashi, M.; Shimizu, T.; Minaka, N.; Akutsu, K.
J. Gen. Virol. 79, 2051-2058, 1998
A:Title: The complete nucleotide sequence of the rice grassy stunt virus genome and
A:Reference number: Z14118; MUID:98378059; PMID:9714257
A:Accession: T00133
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: genomic RNA
A:Residues: 1-2925 <TOR>
A:Cross-references: EMBL:AB009656; NID:g3410897; PIDN:BAA32246.1; PID:g3410899
A:Experimental source: Isolate IRRI
C:Keywords: nucleotidyltransferase

Query Match 53.4%; Score 55.5; DB 2; Length 2925;
Best Local Similarity 64.7%; Pred. No. 11;
Matches 11; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

Qy 1 NPENSRGKGRGRGQGN 17
|||:|||||:|::: 2922

Db 2907 NPPSSRGRRG-RCRS 2922

RESULT 5

H87481
Ribonuclease, Rne/Rng family protein [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: H87481
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Koo, N. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: H87481
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-898 <SPO>
A:Cross-references: GB:AE005673; NID:g13423322; PIDN:AAK23852.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC1877

Query Match 51.9%; Score 54; DB 2; Length 898;
Best Local Similarity 57.9%; Pred. No. 6.5;
Matches 11; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Qy 3 ENSRG--KGRRGQGNRG 19
::| | | | | | | | | |

Db 604 DDERGRKGRGRDRNRG 622

RESULT 6

B48058
RNA-binding protein NAB2 - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein G2910; protein YGL122c
C:Species: Saccharomyces cerevisiae
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 21-Jul-2000
C:Accession: B48058; A48058; S64132
R:Anderson, J.T.; Wilson, S.M.; Datar, K.V.; Swanson, M.S. Mol. Cell. Biol. 13, 2730-2741, 1993
A:Title: NAB2: a yeast nuclear polyadenylated RNA-binding protein essential for cell
A:Reference number: A48058; MUID:93233636; PMID:8474438
A:Accession: B48058
A:Molecule type: DNA
A:Residues: 1-525 <AND>
A:Cross-references: GB:U10288; NID:C295628; PIDN:AAA24819.1; PID:C295628

A:Experimental source: strain B0926
 A:Accession: A48058
 A:Molecule type: DNA
 A:Residues: 1-120,149-525 <ANN>
 A:Cross-references: NID:g295630; PIDN:AAA34820.1; PID:g295631
 A:Experimental source: strain YNN318
 A:Note: sequence extracted from NCBI backbone (NCBIN:129803; NCBI:129804)
 R:Laquin, G.
 submitted to the Protein Sequence Database, May 1996
 A:Reference number: S64122
 A:Accession: S64132
 A:Molecule type: DNA
 A:Residues: 1-525 <DNA>
 A:Cross-references: EMBL:272644; NID:g1322680; PID:e243350; PID:g1322681; MIPS:YGL122c
 A:Experimental source: strain S288C
 C:Genetics:
 A:Gene: SGD:NAB2
 A:Cross-references: SGD:S0003090; MIPS:YGL122c
 A:Map position: 7L
 A:Keywords: nucleus; RNA binding

Query Match 49.0%; Score 51; DB 2; Length 525;
 Best Local Similarity 76.9%; Pred. No. 11;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 GKRRGGRGKNG 19
 || ||| || |||
 Db 215 GKNRRGGGNG 227

RESULT 7
 A97501
 topoisomerase iv chain a [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
 C:Species: Agrobacterium tumefaciens
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
 C:Accession: A97501
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
 Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A:Reference number: A97359; PMID:11743194
 A:Accession: A97501
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-750 <KUR>
 A:Cross-references: GB:AE007869; PIDN:AAK86962.1; PID:g15156198; GSPDB:GN00169
 C:Genetics:
 A:Gene: AGR_C_2144
 A:Map position: circular chromosome
 C:Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomerase

Query Match 49.0%; Score 51; DB 2; Length 750;
 Best Local Similarity 66.7%; Pred. No. 15;
 Matches 12; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 PENSCKGRGGRGKNG 19
 || ||| || |||
 Db 677 PENSCKGVRLQRYKDG 694

RESULT 8
 AE2719
 topoisomerase IV subunit A parC [imported] - Agrobacterium tumefaciens (strain C58, Dup
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
 C:Accession: AE2719
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, H
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; PMID:11743193
 A:Accession: AE2719
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-750 <KUR>
 A:Cross-references: GB:AE008688; PIDN:AA42171.1; PID:g17739560; GSPDB:GN00186
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: parC
 A:Map position: circular chromosome
 C:Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomeras

Query Match 49.0%; Score 51; DB 2; Length 750;
 Best Local Similarity 66.7%; Pred. No. 15;
 Matches 12; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 PENSCKGRGGRGKNG 19
 || ||| || |||
 Db 677 PENSCKGVRLQRYKDG 694

RESULT 9
 E86451
 probable copia-type polyprotein, 28768-32772 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cross)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: E86451
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
 ansen, N.F.; Hughes, B.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
 Rizzo, M.; Rowley, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: E86451
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1334 <STO>
 A:Cross-references: GB:AE005172; NID:g10092575; PIDN:AAG12968.1; GSPDB:GN00141
 C:Genetics:
 A:Map position: 1
 C:Superfamily: retrovirus-related polyprotein

Query Match 49.0%; Score 51; DB 2; Length 1334;
 Best Local Similarity 60.0%; Pred. No. 24;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 SRCKGRGGRGKNG 19
 ||| ||| ||| |||
 Db 228 SRCKGRGGRGGRG 242

RESULT 10
 WMBEL1
 latency-related protein 1 - human herpesvirus 1 (strain F)
 C:Species: human herpesvirus 1
 A:Note: host Homo sapiens (man)
 C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 10-Sep-1999
 C:Accession: A33337
 R:Wechsler, S.L.; Nesburn, A.B.; Zwaagstra, J.; Ghiasi, H.
 Virology 168, 168-172, 1989
 A:Title: Sequence of the latency-related gene of herpes simplex virus type 1.
 A:Reference number: A94388; MUID:89085598; PMID:2535901
 A:Accession: A33337
 A>Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-340 <WEC>
 A:Cross-references: GB:J04323; NID:g330133; PIDN:AAA45799.1; PID:g330134
 C:Genetics:

A:Introns: 249/2
 C:Superfamily: herpesvirus latency-related protein 1
 C:Keywords: tandem repeat
 F:26-41/Region: 16-residue tandem repeat
 F:42-57/Region: 16-residue tandem repeat
 F:58-73/Region: 16-residue tandem repeat

Query Match 48.1%; Score 50; DB 1; Length 340;
 Best Local Similarity 50.0%; Pred. No. 10;
 Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 PENSCKGRRGQGRGKNG 19
 | ||| ||| ||| |||
 Db 305 PRGSRGGRGGRGGRGG 322

RESULT 11
 F64056
 Probable ATP-dependent RNA helicase - Haemophilus influenzae (strain Rd KW20)
 C:Species: Haemophilus influenzae
 C:Note: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 02-Feb-2001
 C:Accession: F64056
 R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M. Science 269, 496-512, 1995
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.
 A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
 A:Reference number: A64000; MUID:95350630; PMID:7542800
 A:Accession: F64056
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-613 <TIGR>
 A:Cross-references: GB:U32709; GB:L42023; NID:g1573190; PIDN:RAC21900.1; PID:g1573195; T
 C:Keywords: ATP; nucleotide binding; P-loop
 F:49-56/Region: nucleotide-binding motif A (P-loop)
 F:151-156/Region: nucleotide-binding motif B
 F:155-158/Region: DEAD motif

Query Match 48.1%; Score 50; DB 2; Length 613;
 Best Local Similarity 44.8%; Pred. No. 17;
 Matches 13; Conservative 3; Mismatches 1; Indels 12; Gaps 2;

QY 3 ENSRG-----KGR-----RGQRGKNG 19
 |||||
 Db 556 DNSRGSDDFNGKRGGRGGRGREG 584

RESULT 12
 F64058
 Hypothetical protein F2401.20 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Mar-2001
 C:Accession: T01458
 R:Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Cor
 eologis, A.; Ecker, J.R.
 submitted to the EMBL Data Library, January 1998
 A:Description: Genomic sequence for Arabidopsis thaliana BAC F2401.
 A:Reference number: Z14211
 A:Accession: T01458
 A:Status: translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-296 <SHI>
 A:Cross-references: EMBL:AC003113; NID:g26899438; PID:g2781364; GSPDB:GN00059; ATSP:F2401
 C:Genetics:
 A:Gene: ATSP:F2401.20
 A:Map position: 1

Query Match 47.6%; Score 49.5; DB 2; Length 296;
 Best Local Similarity 68.8%; Pred. No. 10;
 Matches 11; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

QY 4 NSRGKGRGQGRGKNG 19

Db 242 NSRGGRSQ---NRG 254
 ||||| ||| |||

RESULT 13
 AH1867
 Hypothetical protein alr0489 [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp.
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
 C:Accession: AH1867
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigui
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AH1867
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-893 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BAW72447.1; PID:g17129834; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: alr0489
 C:Superfamily: yeast probable SKI2 protein YUL050w

Query Match 47.6%; Score 49.5; DB 2; Length 893;
 Best Local Similarity 61.1%; Pred. No. 28;
 Matches 11; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 1 NPE-NSRGKGRGQGRGKNG 17
 || ||| ||| ||| |||
 Db 224 NPRLNRGKRGQGRGKNG 241

RESULT 14
 T39586
 rna binding protein - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T39586
 R:Volckaert, G.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, August 1997
 A:Reference number: Z21865
 A:Accession: T39586
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-166 <VOL>
 A:Cross-references: EMBL:Z99759; PIDN:CAB16904.1; GSPDB:GN00067; SPDB:SPBC16E9.12c
 A:Experimental source: strain 972h-; cosmid c16E9
 C:Genetics:
 A:Gene: SPDB:SPBC16E9.12c
 A:Map position: 2
 A:Introns: 12/3; 97/2; 126/3

Query Match 47.1%; Score 49; DB 2; Length 166;
 Best Local Similarity 55.6%; Pred. No. 7.3;
 Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 PENSCKGRRGQGRGKNG 19
 | ||| ||| ||| |||
 Db 135 PGMSRGGRGGRGGRGGRG 152

RESULT 15
 S36541
 E2 protein - human papillomavirus type 12
 C:Species: human papillomavirus type 12
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
 C:Accession: S36541
 R:Deilus, H.; Hofmann, B.
 submitted to the EMBL Data Library, August 1993
 A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469
A:Accession: S36541
A:Molecule type: DNA
A:Residues: 1-494
A:Cross-references: EMBL:X74466; NID:g396910; PIDN:CAA52499.1; PID:g396914
C:Superfamily: papillomavirus E2 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match	47.1%	Score 49;	DB 2;	Length 494;
Best Local Similarity	69.2%	Pred. No. 19;		
Matches 9;	Conservative 1;	Mismatches 3;	Indels 0;	Gaps 0;

OY 6 RKGRRGQGGKNR 18
||:| || ||| |
Db 344 RGRGRRGGRKR 356

Search completed: December 4, 2002, 08:19:16
Job time : 18 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 08:15:32 ; Search time 10 Seconds
(without alignments)
78.805 Million cell updates/sec

Title: US-09-687-993-18
Perfect score: 104
Sequence: 1 NPENSRGKRGQRQKNG 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

atched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	104	100.0	211	1 GDNF_HUMAN	P39905 homo sapien
2	99	95.2	211	1 GDNF_MOUSE	P48540 mus musculu
3	99	95.2	211	1 GDNF_RAT	Q07731 rattus norv
4	94	91.9	708	1 MR11_HUMAN	P49959 homo sapien
5	51.5	49.5	894	1 ILF3_HUMAN	Q12906 h interleuk
6	51.5	49.5	910	1 ILF3_RAT	Q9j1l3 rattus norv
7	51.5	49.5	911	1 ILF3_MOUSE	Q921x4 mus musculu
8	51	49.0	525	1 NAB2_YEAST	P32505 saccharomyc
9	50	48.1	265	1 RS2_LETAM	O43992 leishmania
10	50	48.1	340	1 LRP1_HSV1F	P17588 herpes simp
11	50	48.1	613	1 DEAD_HAEIN	P44586 haemophilus
12	49	47.1	494	1 VE2_HPV12	P36782 human papil
13	48.5	46.6	633	1 ROR_HUMAN	O43390 homo sapien
14	48.5	46.6	643	1 YK09_CAEEL	P34304 caenorhabdi
15	48	46.2	126	1 SMD1_CAEEL	Q10013 caenorhabdi
16	48	46.2	758	1 PARC_RHIME	Q59749 rhizobium m
17	47.5	45.7	117	1 SMD1_SCHPO	O42661 schizosacch
18	47	45.2	706	1 MR11_MOUSE	Q61216 mus musculu
19	46	44.2	65	1 Y214_TREPA	O83244 treponema p
20	46	44.2	321	1 FBRL_HUMAN	P22087 homo sapien
21	46	44.2	551	1 CC14_YEAST	Q00684 saccharomyc
22	46	44.2	632	1 FMRI_HUMAN	Q06787 homo sapien
23	46	44.2	706	1 MR11_RAT	Q9j1m0 rattus norv
24	45.5	43.8	123	1 LSM4_CAEEL	Q19952 caenorhabdi
25	45	43.3	178	1 VP12_WTVNJ	P31612 wound tumor
26	45	43.3	253	1 RS2_SCHPO	O74892 schizosacch
27	45	43.3	707	1 RHO_STRLI	P52157 streptomyce
28	45	43.3	862	1 TP3B_MOUSE	Q9z321 mus musculu
29	44.5	42.8	153	1 IF1A_YEAST	P38912 saccharomyc
30	44.5	42.8	414	1 NSR1_YEAST	P27476 saccharomyc
31	44.5	42.8	700	1 MR11_CHICK	Q9iam7 gallus gall
32	44	42.3	483	1 VE2_HPV14	P36783 human papil
33	44	42.3	720	1 MR11_ARATH	Q9xgm2 arabidopsis

RESULT 1				
GDNF_HUMAN				
ID	GDNF_HUMAN	STANDARD;	PRT;	211 AA.
AC	P39905; Q9UP97; Q9UD33;			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Glial cell line-derived neurotrophic factor precursor (Astrocyte-			
DE	derived trophic factor 1) (ATF-1).			
GN	GDNF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=93262463; PubMed=8493557;			
RA	Lin L. F.H.; Boherty D.H.; Lille J.D., Bektesh S., Collins F.;			
RT	"GDNF: a glial cell line-derived neurotrophic factor for midbrain			
RT	dopaminergic neurons.";			
RL	Science 260:1130-1132(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RX	MEDLINE=95172201; PubMed=7867768;			
RA	Schaar D.G., Steber B.A., Sherwood A.C., Dean D., Mendoza G.,			
RA	Ramakrishnan L., Dreyfus C.F., Black I.B.;			
RT	"Multiple astrocyte transcripts encode nigral trophic factors in rat			
RT	and human.";			
RL	Exp. Neurol. 130:387-393(1994).			
RN	[3]			
RP	SEQUENCE OF 1-187 FROM N.A. (ISOFORM 1).			
RC	TISSUE=Kidney;			
RX	MEDLINE=99296655; PubMed=10366742;			
RA	Baecker P.A., Lee W.H., Verity A.N., Eglen R.M., Johnson R.M.;			
RT	"Characterization of a promoter for the human glial cell line-derived			
RT	neurotrophic factor gene.";			
RL	Brain Res. Mol. Brain Res. 69:209-222(1999).			
RN	[4]			
RP	PARTIAL SEQUENCE, AND DISULFIDE BONDS.			
RX	MEDLINE=97141760; PubMed=898018;			
RA	Haniu M., Hui J., Young Y., Le J., Katta V., Lee R., Shimamoto G.,			
RA	Rohde M.F.;			
RT	"Glial cell line-derived neurotrophic factor: selective reduction of			
RT	the intermolecular disulfide linkage and characterization of its			
RT	disulfide structure.";			
RL	Biochemistry 35:16799-16805(1996).			
RN	[5]			
RP	REVIEW ON VARIANTS.			
RX	MEDLINE=98023959; PubMed=9359036;			
RA	Hofstra R.M.W., Osinga J., Buys C.H.C.M.;			
RT	"Mutations in Hirschsprung disease: when does a mutation contribute to			
RT	the phenotype.";			
RL	Eur. J. Hum. Genet. 5:180-185(1997).			
RN	[6]			
RP	VARIANT HSCR SER-154.			
RX	MEDLINE=97123511; PubMed=8968758;			

Q15027 homo sapien
P22082 saccharomyc
Q09003 xenopus lae
P13941 rattus norv
P08121 mus musculu
P34486 caenorhabdi
Q27294 drosophila
Q9JY25 neisseria m
Q9K012 neisseria m
P12978 epstein-bar
P26545 human papil
P27565 sendai viru

RA Ivanchuk S.M., Myers S.M., Eng C., Mulligan L.M.;
 RT "De novo mutation of GDNF, ligand for the RET/GDNFR-alpha receptor
 RL complex, in Hirschsprung disease.";
 RN Hum. Mol. Genet. 5:2023-2026(1996).
 RN VARIANT HSCR TRP-93.
 RX MEDLINE=97051933; PubMed=8896568;
 RA Angrist M., Bolk S., Halushka M., Lapchak P.A., Chakravarti A.;
 RT "Germline mutations in glial cell line-derived neurotrophic factor
 RL (GDNF) and RET in a Hirschsprung disease patient.";
 RN Nat. Genet. 14:341-344(1996).
 RN [8]
 RN VARIANTS HSCR SER-21 AND ASN-150.
 RX MEDLINE=97051934; PubMed=8896569;
 RA Salomon R., Attie T., Pellet A., Bidaud C., Eng C., Amiel J.,
 RA Sarnacki S., Goulet O., Ricour C., Nihoul-Fekete C., Munnich A.,
 RA Lyonnet S.;
 RT "Germline mutations of the RET ligand GDNF are not sufficient to cause
 RL Hirschsprung disease.";
 RN Nat. Genet. 14:345-347(1996).
 CC -1- FUNCTION: NEUROTROPHIC FACTOR THAT ENHANCES SURVIVAL AND
 MORPHOLOGICAL DIFFERENTIATION OF DOPAMINERGIC NEURONS AND
 INCREASES THEIR HIGH-AFFINITY DOPAMINE UPTAKE.
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- DISEASE: IN ASSOCIATION WITH MUTATIONS OF RET GENE, MAY BE
 INVOLVED IN HIRSCHSPRUNG'S DISEASE (HSCR). THIS GENETIC DISORDER
 CC OF NEURAL CREST DEVELOPMENT IS CHARACTERIZED BY THE ABSENCE OF
 CC INTRAMURAL GANGLION CELLS IN THE HINDGUT; OFTEN RESULTING IN
 CC INTESTINAL OBSTRUCTION.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY. GDNF SUBFAMILY.
 CC -1- DATABASE: NAME-RD Systems' cytokine mini-reviews: GDNF;
 CC WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyid=201".
 CC -----
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 CC -----
 DR EMBL: L19063; AAA67910.1; -
 DR EMBL: L19062; AAA67910.1; JOINED.
 DR EMBL: AF053748; AAD43139.1; -
 DR PIR: B37499; B37499.
 DR HSP: Q07731; IAGO.
 DR Genew: HGNC:4232; GDNF.
 DR MIM: 600837; -
 DR MIM: 142623; -
 DR InterPro: IPR001839; TGFb.
 DR Pfam: PF00019; TGF-beta; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF_BETA_1; FALSE NEG.
 DR Growth factor; Glycoprotein; Signal: Alternative splicing;
 KW Polymorphism; Disease mutation; Hirschsprung disease.
 FT SIGNAL 1 19 POTENTIAL.
 FT PROPEP 20 77 BY SIMILARITY.
 FT CHAIN 78 211 GLIAL CELL LINE-DERIVED NEUROTROPHIC
 FACTOR.
 FT FT
 FT DISULFID 118 179
 FT DISULFID 145 208
 FT DISULFID 149 210
 FT DISULFID 178 210
 FT DISULFID 178 210
 FT CARBOHYD 126 126
 FT CARBOHYD 162 162
 FT VARSPLIC 25 51
 FT FT
 FT VARIANT 21 21
 FT P->S (IN HSCR; COULD BE A
 FT POLYMORPHISM).
 FT /FTID-VAR_009494.
 FT FT

FT VARIANT 93 93 R -> W (IN HSCR; ASSOCIATED TO A RET
 FT MUTATION; COULD BE AN EXTREMELY RARE
 FT POLYMORPHISM).
 FT /FTID-VAR_009495.
 FT D -> N (IN HSCR; COULD BE A
 FT POLYMORPHISM).
 FT /FTID-VAR_009496.
 FT T -> S (IN HSCR; SPORADIC FORM).
 FT /FTID-VAR_009497.
 FT SEQUENCE 211 AA; 23720 MW; A0D1EBF77FC82691 CRC64;
 SQ
 Query Match 100.0%; Score 104; DB 1; Length 211;
 Best Local Similarity 100.0%; Pred. No. 4e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NPENSRGKGRGGRGKNGR 19
 Db 99 NPENSRGKGRGGRGKNGR 117
 |||||
 RESULT 2
 GDNF_MOUSE STANDARD; PRT; 211 AA.
 ID GDNF_MOUSE P48540; P97919; O09058; P97920; P70446;
 AC P48540; P97919; O09058; P97920; P70446;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Glial cell line-derived neurotrophic factor precursor.
 GN GDNF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN=C57BL/10J; TISSUE=Brain;
 RA Wang F., Too H.P.;
 RN Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR; TISSUE=Dorsal root ganglion;
 RX MEDLINE=95379105; PubMed=7650763;
 RA Watabe K., Fukuda T., Tanaka J., Honda H., Toyohara K., Sakai O.;
 RT "Spontaneously immortalized adult mouse Schwann cells secrete
 RT autocrine and paracrine growth-promoting activities.";
 RN J. Neurosci. Res. 41:279-290(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ;
 RA Hellmich H., Kos L., Cho E.S., Mahon K.A., Zimmer A.;
 RN Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Matsushita N., Fujita Y., Nagatsu T., Kiuchi K.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: NEUROTROPHIC FACTOR THAT ENHANCES SURVIVAL AND
 MORPHOLOGICAL DIFFERENTIATION OF DOPAMINERGIC NEURONS AND
 INCREASES THEIR HIGH-AFFINITY DOPAMINE UPTAKE.
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY. GDNF SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: U37459; AAB18672.1; ALT_INIT.
 DR


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DR EMBL; U66195; AAB07463.1; ALT_INIT.
DR EMBL; U75532; AAB18343.1; ALT_INIT.
DR EMBL; D49921; BAA08660.1; -.
DR EMBL; U36449; AAB52953.1; -.
DR EMBL; D88264; BAA13566.1; ALT_INIT.
DR EMBL; D88352; BAB12221.1; -.
DR EMBL; D88351; BAB12221.1; JOINED.
DR HSSP; Q07731; IAGQ.
DR MGD; MGI:107430; Gdnf.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF-beta; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; FALSE_NEG.
KW Growth factor; Glycoprotein; Signal; Alternative splicing.
FT SIGNAL 1 19
FT PROPEP 20 77
FT CHAIN 78 211
FT DISULFID 118 179
FT DISULFID 145 208
FT DISULFID 149 210
FT DISULFID 178 178
FT CARBOHYD 126 126
FT CARBOHYD 162 162
FT VARSPPLIC 25 51
FT SEQUENCE 211 AA; 23662 MW; B6731C767A3A95B7 CRC64;

Query Match 95.2%; Score 99; DB 1; Length 211;
Best Local Similarity 94.7%; Pred. No. 2.1e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPENSRGKGRGGRGKNGR 19
Db :|||||
99 SPENSRGKGRGGRGKNGR 117

RESULT 3
GNF_RAT STANDARD; PRT; 211 AA.
AC Q07731; Q64062; Q63214;
DT 01-FEB-1995 (Rel. 31, Created);
DT 01-FEB-1995 (Rel. 31, Last sequence update);
DT 16-OCT-2001 (Rel. 40, Last annotation update);
DE Glial cell line-derived neurotrophic factor precursor.
GN GDNF.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 78-102.
RX MEDLINE-93262463; PubMed-8493557;
RA Lin L.-F.H., Doherty D.H., Lille J.D., Bektesh S., Collins F.;
*GDNF: a glial cell line-derived neurotrophic factor for midbrain
RT dopaminergic neurons.*;
RL Science 260:1130-1132(1993).
RN [2]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE-95203379; PubMed-7895811;
RA Springer J.E., Seeburger J.B., He J., Gabrea A., Blankenhorn E.P.,
Bergman L.W.;
*CDNA sequence and differential mRNA regulation of two forms of glial
RT cell line-derived neurotrophic factor in Schwann cells and rat
skeletal muscle.*;
RL Exp. Neurol. 131:47-52(1995).
RN [3]
SEQUENCE OF 1-50 FROM N.A., AND ALTERNATIVE SPLICING.
RP STRAIN-Wistar; TISSUE-Kidney;
RX MEDLINE-95210610; PubMed-7656586;
RA Suter-Crazzolara C., Unsicker K.;
*GDNF is expressed in two forms in many tissues outside the CNS.*;
RL NeuroReport 5:2486-2488(1994).

RN [4]
ALTERNATIVE SPLICING.
RX MEDLINE-95172201; PubMed-7867768;
RA Schaar D.G., Sieber B.A., Sherwood A.C., Dean D., Mendoza G.,
Ramakrishnan L., Dreyfus C.F., Black I.B.;
*Multiple astrocyte transcripts encode nigral trophic factors in rat
RT and human.*;
RL Exp. Neurol. 130:387-393(1994).
RN [5]
X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE-97331316; PubMed-9187648;
RA Eigenbrot C., Gerber C.;
*X-ray structure of glial cell-derived neurotrophic factor at 1.9-A
RT resolution and implications for receptor binding.*;
RL Nat. Struct. Biol. 4:435-438(1997).
CC -1- FUNCTION: NEUROTROPHIC FACTOR THAT ENHANCES SURVIVAL AND
MORPHOLOGICAL DIFFERENTIATION OF DOPAMINERGIC NEURONS AND
INCREASES THEIR HIGH-AFFINITY DOPAMINE UPTAKE.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1/GDNF633 (SHOWN HERE) AND
2/GDNF555; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY. GDNF SUBFAMILY.
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DR EMBL; L15305; AAB67909.1; -.
DR EMBL; S75583; AAB33891.1; -.
DR EMBL; S75585; AAB33892.1; -.
DR EMBL; X92495; CAA63237.1; -.
DR PIR; A37499; A37499.
DR PDB; IAGQ; 05-JUN-97.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF-beta; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; FALSE_NEG.
KW Growth factor; Glycoprotein; Signal; Alternative splicing;
3D-structure.
FT SIGNAL 1 19
FT PROPEP 20 77
FT CHAIN 78 211
FT DISULFID 118 179
FT DISULFID 145 208
FT DISULFID 149 210
FT DISULFID 178 178
FT CARBOHYD 126 126
FT CARBOHYD 162 162
FT VARSPPLIC 25 51
FT CONFLICT 77 77
FT CONFLICT 90 90
FT CONFLICT 101 101
FT CONFLICT 211 AA; 23619 MW; AE06C646682895A5 CRC64;
SQ SEQUENCE 211 AA; 23619 MW; AE06C646682895A5 CRC64;

Query Match 95.2%; Score 99; DB 1; Length 211;
Best Local Similarity 94.7%; Pred. No. 2.1e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPENSRGKGRGGRGKNGR 19
Db :|||||
99 SPENSRGKGRGGRGKNGR 117

RESULT 4
MR11_HUMAN STANDARD; PRT; 708 AA.
ID MR11_HUMAN

```

AC P49959; O43475;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Double-strand break repair protein MRE11A (MRE11 homolog 1).
 DE MRE11A OR MRE11 OR HNGS1.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN MEDLINE=96079094; PubMed=8530104;
 RX Petrini J.H.J., Walsh M.E., Dimare C., Chen X.-N., Korenberg J.R.,
 RA Weaver D.T.;
 RA "Isolation and characterization of the human MRE11 homologue.";
 RL Genomics 29:80-86(1995).
 RN [2]
 RN REVISIONS TO C-TERMINUS.
 RA Petrini J.H.J., Walsh M.E., Dimare C., Chen X.-N., Korenberg J.R.,
 RA Weaver D.T.;
 RA Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RA Chamankhah M., Wei Y., Xiao W.;
 RA "Molecular cloning and functional characterization of hNGS1, a yeast
 RT and human MRE11 homolog.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=98315380; PubMed=9651580;
 RA Pauli T.T., Gellert M.;
 RA "The 3' to 5' exonuclease activity of Mre 11 facilitates repair of DNA
 RT double-strand breaks.";
 RL Mol. Cell 1:969-979(1998).
 RN [5]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=21364328; PubMed=11371508;
 RA Pitts S.A., Kullar H.S., Stankovic T., Stewart G.S., Last J.I.K.,
 RA Bedenham T., Armstrong S.J., Plane M., Chessa L., Taylor A.M.R.,
 RA Byrd P.J.;
 RA "hMRE11: genomic structure and a null mutation identified in a
 RT transcript protected from nonsense-mediated mRNA decay.";
 RL Hum. Mol. Genet. 10:1155-1162(2001).
 RN [6]
 RN VARIANT ATLD SER-117.
 RX MEDLINE=20077641; PubMed=10612394;
 RA Stewart G.S., Maser R.S., Stankovic T., Bressan D.A., Kaplan M.I.,
 RA Jaspers N.G.J., Raams A., Byrd P.J., Petrini J.H.J., Taylor A.M.R.;
 RA "The DNA double-strand break repair gene hMRE11 is mutated in
 RT individuals with an ataxia-telangiectasia-like disorder.";
 RL Cell 99:577-587(1999).
 RN [7]
 RN VARIANTS.
 RX MEDLINE=21036682; PubMed=11196167;
 RA Fukuda T., Sumiyoshi T., Takahashi M., Kataoka T., Asahara T.,
 RA Inui H., Watanabe M., Yasutomi M., Kanada N., Miyagawa K.;
 RA "Alterations of the double-strand break repair gene MRE11 in cancer.";
 RL Cancer Res. 61:23-26(2001).
 CC -!- FUNCTION: Involved in DNA double-strand break repair (DSBR).
 CC Possesses single-strand endonuclease activity and double-strand-
 CC specific 3'-5' exonuclease activity. Also involved in meiotic DSB
 CC processing.
 CC -!- COFACTOR: Manganese (By similarity).
 CC -!- SUBUNIT: FORMS A COMPLEX WITH RAD50 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC -!- DISEASE: DEFECTS IN MRE11A ARE A CAUSE OF ATAXIA-TELANGIECTASIA-
 CC LIKE DISORDER (ATLD). IT IS A DISEASE WITH THE SAME CLINICAL
 CC FEATURE THAN ATAXIA-TELANGIECTASIA BUT WITH A SOMEWHAT Milder
 CC CLINICAL COURSE.
 CC -!- SIMILARITY: BELONGS TO THE MRE11/RAD32 FAMILY.

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 CC -----
 DR EMBL: U37359; AAC78721.1; -;
 DR EMBL: AF022778; AAD10197.1; -;
 DR EMBL: AF073362; AAC36249.1; -;
 DR EMBL: AF303395; AAK18790.1; -;
 DR EMBL: AF303379; AAK18790.1; JOINED.
 DR EMBL: AF303380; AAK18790.1; JOINED.
 DR EMBL: AF303381; AAK18790.1; JOINED.
 DR EMBL: AF303382; AAK18790.1; JOINED.
 DR EMBL: AF303383; AAK18790.1; JOINED.
 DR EMBL: AF303384; AAK18790.1; JOINED.
 DR EMBL: AF303385; AAK18790.1; JOINED.
 DR EMBL: AF303386; AAK18790.1; JOINED.
 DR EMBL: AF303387; AAK18790.1; JOINED.
 DR EMBL: AF303388; AAK18790.1; JOINED.
 DR EMBL: AF303389; AAK18790.1; JOINED.
 DR EMBL: AF303390; AAK18790.1; JOINED.
 DR EMBL: AF303391; AAK18790.1; JOINED.
 DR EMBL: AF303392; AAK18790.1; JOINED.
 DR EMBL: AF303393; AAK18790.1; JOINED.
 DR EMBL: AF303394; AAK18790.1; JOINED.
 DR Genew: HGNC:7230; MRE11A.
 DR MIM: 604391; -;
 DR InterPro: IPR003701; DNA_repair.
 DR InterPro: IPR004843; M-ppetrase.
 DR InterPro: IPR004844; S/T-phosphatase.
 DR Pfam: PF00149; Metallophos; 1.
 DR TIGRFAMs: TIGR00583; mre11; 1.
 KW DNA repair; Hydrolase; Nuclease; Endonuclease; Exonuclease;
 KW Nuclear protein; Manganese; Meiosis; Alternative splicing;
 KW Disease mutation; Polymorphism.
 FT VARSPLIC 595 622 MISSING (IN ISOFORM 2).
 FT VARIANT 104 104 S -> C (IN CANCER).
 FT VARIANT 117 117 N -> S (IN ATLD).
 FT VARIANT 157 157 /FTID-VAR_008513.
 FT VARIANT 503 503 /FTID-VAR_011626.
 FT VARIANT 572 572 /FTID-VAR_011627.
 FT VARIANT 572 572 R -> O (IN CANCER).
 FT CONFLICT 31 31 /FTID-VAR_011628.
 FT CONFLICT 31 31 V -> A (IN REF. 1).
 SQ SEQUENCE 708 AA; 80593 MW; D94ABFDDF6106AD CRC64;
 Query Match 51.9%; Score 54; DB 1; Length 708;
 Best Local Similarity 58.8%; Pred. No. 1.8;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 OY 1 NPENSRGKGRRGGRGKN 17
 DB 567 NKGRGRGRGRGRGKN 563
 RESULT 5
 ILF3_HUMAN STANDARD; PRT; 894 AA.
 ID Q12906; Q9UN84; Q9NQ95; Q9NQ96; Q9NQ97; Q9NQ98; Q9NQ99; Q9NQAO;
 AC Q9NQAO1; Q9NQAO2; Q9NQAO3; Q9NQAO4; Q9NQAO5; Q9NB2H4; Q9NB2H5; Q99544;
 AC Q99545; Q9NRN2; Q9NRN3; Q9NRN4; O43409;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin enhancer-binding factor 3 (Nuclear factor of activated T

DE cells-90) (NF-AT-90) (Double-stranded RNA-binding protein 76) (DRBP76)
DE (Translational control protein 80) (TCP80) (Nuclear factor associated
DE with GARN) (NFAF) (W-phase phosphoprotein 4) (MPP4).
GN ILF3 OR NF90 OR DRBF OR MPOSPH4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PRELIMINARY SEQUENCE FROM N.A., AND SEQUENCE OF 19-41; 491-510 AND
RP 555-565.
RC TISSUE=T-cell lymphoma;
RX MEDLINE=94327652; PubMed=7519613;
RA Kao P.N., Chen L., Brock G., Ng J., Kenny J., Smith A.J., Cortesby B.;
RT "Cloning and expression of cyclosporin A- and FK506-sensitive nuclear
RT factor of activated T-cells: NF45 and NF90.";
RL J. Biol. Chem. 269:20691-20699(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND SEQUENCE OF N-TERMINUS.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=99329057; PubMed=10400669;
RA Patel R.C., Vestal D.J., Xu Z., Bandyopadhyay S., Guo W., Erme S.M.,
RA Williams B.R., Sen G.C.;
RT "DRBP76, a double-stranded RNA-binding nuclear protein, is
RT phosphorylated by the interferon-induced protein kinase, PKR.";
RL J. Biol. Chem. 274:20432-20437(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 3), AND CHARACTERIZATION.
RC TISSUE=Liver;
RX MEDLINE=20076798; PubMed=10607473;
RA Xu Y.-H., Grabowski G.A.;
RT "Molecular cloning and characterization of a translational inhibitory
RT protein that binds to coding sequences of human acid beta-glucosidase
RT and other mRNAs.";
RL Mol. Genet. Metab. 68:441-454(1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 4 AND 5), AND ALTERNATIVE SPLICING.
RC TISSUE=Melanoma;
RX MEDLINE=21100430; PubMed=11167023;
RA Duchange N., Pidoux J., Canus E., Sauvaget D.;
RT "Alternative splicing in the human interleukin enhancer binding factor
RT 3 (ILF3) gene.";
RL Gene 261:345-353(2000).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND CHARACTERIZATION.
RC MEDLINE=21402983; PubMed=11438536;
RX Saunders L.R., Perkins D.J., Balachandran S., Michaels R., Ford R.,
RX Mayeda A., Barber G.N.;
RT "Characterization of two evolutionarily conserved, alternatively
RT spliced nuclear phosphoproteins, NFAR-1 and -2, that function in mRNA
RT processing and interact with the double-stranded RNA-dependent
RT protein kinase, PKR.";
RL J. Biol. Chem. 276:32300-32312(2001).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=T-cell;
RX PubMed=11161820;
RA Saunders L.R., Juretic V., Barber G.N.;
RT "The 90- and 110-kDa human NFAR proteins are translated from two
RT differentially spliced mRNAs encoded on chromosome 19p13.";
RL Genomics 71:256-259(2001).
RN [7]
RP SEQUENCE OF 1-611 FROM N.A.
RC TISSUE=Cervix, and Blood;
RX MEDLINE=97039687; PubMed=8885239;
RA Matsumoto-Taniura N., Pirollet F., Monroe R., Gerace L.,
RA Westendorf J.M.;
RT "Identification of novel M phase phosphoproteins by expression
RT cloning.";
RL Mol. Biol. Cell 7:1455-1469(1996).
RN [8]
RP SEQUENCE OF 188-894 FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MacArdle J., Cantarella G.M., Veyrune J.-L., Krasnoselskaya I.,
Kumar A.;
RT "Structure and functional characterization of IDRBF gene.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE OF 587-894 FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RA Yu W., Sarginson J., Gibbs R.A.;
RT Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [10]
RP INTERACTION WITH HRM1L2.
RX MEDLINE=20347897; PubMed=10749851;
RA Tang J., Kao P.N., Herschman H.R.;
RT "Protein-arginine methyltransferase I, the predominant
RT protein-arginine methyltransferase in cells, interacts with and is
RT regulated by interleukin enhancer-binding factor 3.";
RL J. Biol. Chem. 275:19866-19876(2000).
CC -!- FUNCTION: May facilitate double-stranded RNA-regulated gene
CC expression at the level of post-transcription. Can act as a
CC translation inhibitory protein which binds to coding sequences of
CC acid beta-glucosidase (GCase) and other mRNAs and functions at the
CC initiation phase of GCase mRNA translation, probably by inhibiting
CC its binding to polysomes. Can regulate protein arginine N-
CC methyltransferase 1 activity.
CC -!- SUBUNIT: Interacts with FUS and SMN proteins and also with
CC HRM1L2.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS: 5 isoforms; 1/NFAR-2/ILF3-E (shown here),
CC 2/NFAR-1/DRBP76, 3, 4/DRBP76 Alpha/ILF3-A and 5/DRBP76
CC Delta/Gamma/ILF3-C; are produced by alternative splicing.
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- PTM: Phosphorylated by RNA-dependent protein kinase (PKR).
CC -!- PTM: Methylated by protein arginine N-methyltransferase 1.
CC -!- SIMILARITY: CONTAINS 2 DBM (DOUBLE-STRANDED RNA-BINDING) DOMAINS.
CC -!- CAUTION: Ref.1 sequence differs from that shown due to sequencing
CC errors.
CC -----
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CC -----
DR EMBL; U10324; AAA20994.1; ALT_SEQ.
DR EMBL; AF147209; RAD33966.1;
DR EMBL; AF141870; RAD37575.1;
DR EMBL; AJ271743; CAC01121.1;
DR EMBL; AJ271741; CAC01122.1;
DR EMBL; AJ271741; CAC01123.1;
DR EMBL; AJ271741; CAC01124.1;
DR EMBL; AJ271744; CAC01404.1;
DR EMBL; AJ271745; CAC01405.1;
DR EMBL; AJ271746; CAC01406.1;
DR EMBL; AJ271747; CAC01407.1;
DR EMBL; AF167569; RAD51098.1;
DR EMBL; AF167570; RAD51099.1;
DR EMBL; AF320244; AAK07424.1;
DR EMBL; AF320228; AAK07424.1; JOINED.
DR EMBL; AF320229; AAK07424.1; JOINED.
DR EMBL; AF320230; AAK07424.1; JOINED.
DR EMBL; AF320231; AAK07424.1; JOINED.
DR EMBL; AF320232; AAK07424.1; JOINED.
DR EMBL; AF320233; AAK07424.1; JOINED.
DR EMBL; AF320234; AAK07424.1; JOINED.
DR EMBL; AF320235; AAK07424.1; JOINED.
DR EMBL; AF320236; AAK07424.1; JOINED.
DR EMBL; AF320237; AAK07424.1; JOINED.
DR EMBL; AF320238; AAK07424.1; JOINED.
DR EMBL; AF320239; AAK07424.1; JOINED.
DR EMBL; AF320240; AAK07424.1; JOINED.
DR EMBL; AF320241; AAK07424.1; JOINED.
DR EMBL; AF320242; AAK07424.1; JOINED.

DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE 40S ribosomal protein S2.
 OS Leishmania amazonensis.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5659;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LV78;
 RA Stewart J.C., Heard P.L., Chaudhuri G.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC 1- SIMILARITY: BELONGS TO THE S5P FAMILY OF RIBOSOMAL PROTEINS.
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 CC -----
 CC EMBL: AF038379; AAB94922.1; -
 DR HSSP: P02357; LKRP.
 DR InterPro: IPR000851; Ribosomal_S5.
 DR InterPro: IPR005324; Ribosomal_S5_C.
 DR Pfam: PF00333; Ribosomal_S5; 1.
 DR Pfam: PF03719; Ribosomal_S5_C; 1.
 DR TIGRFAMs: TIGR01020; rpsE_arch; 1.
 DR PROSITE: PS00585; RIBOSOMAL_S5; 1.
 DR Ribosomal protein.
 KW Ribosomal protein.
 SQ SEQUENCE 265 AA; 28703 MW; 8D704D3360D45B22 CRC64;

 Query Match 48.1%; Score 50; DB 1; Length 265;
 Best Local Similarity 64.3%; Pred. No. 2.5;
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

 QY 6 RGRGRRGGRGKNGR 19
 ||:| | | | | | |
 DB 24 RGRGRRGGRGGRG 37

 RESULT 10
 LRPL_HSVIF
 ID LRPL_HSVIF STANDARD; PRT; 340 AA.
 AC P17588;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Latency-related protein 1.
 OS Herpes simplex virus (type 1 / strain F).
 OS Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OS Alphaherpesvirinae; Simplexvirus.
 OX NCBI_TaxID=10304;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89085598; PubMed=2535901;
 RA Wechsler S.L., Nesburn A.B., Zwaagstra J., Ghiasi H.;
 RT "Sequence of the latency-related gene of herpes simplex virus type
 RT 1."
 RL Virology 168:168-172(1989).
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 CC -----
 CC EMBL: J04323; AAA45799.1; -
 DR PIR: A33337; WNBEL1.
 DR Repeat.
 KW DOMAIN
 FT REPEAT 27 75 2 x 17 AA REPEATS.
 FT 27 43 1.

FT REPEAT 59 75 2.
 SQ SEQUENCE 340 AA; 35604 MW; 2977FA8F887E5451 CRC64;

 Query Match 48.1%; Score 50; DB 1; Length 340;
 Best Local Similarity 50.0%; Pred. No. 3.2;
 Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

 QY 2 PENSRRGRRGGRGKNGR 19
 | | | | | | | | | |
 DB 305 PRGSRGRRGGRGGRGG 322

 RESULT 11
 DEAD_HAEIN
 ID DEAD_HAEIN STANDARD; PRT; 613 AA.
 AC P44586;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cold-shock DEAD-box protein A homolog (ATP-dependent RNA helicase dead
 DE homolog).
 GN DEAD OR CSDA OR HI0231.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Rd / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
 RT Rd."
 RL Science 269:496-512(1995).
 CC 1- FUNCTION: HAS A HELIX-DESTABILIZING ACTIVITY (BY SIMILARITY).
 CC 1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC 1- SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY.
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 CC -----
 CC EMBL: U32709; AAC21900.1; -
 DR HSSP: Q58083; 1HV8.
 DR TIGR: HI0231; -
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR000629; DEAD_box.
 DR InterPro: IPR001650; Helicase_C.
 DR Pfam: PF00270; DEAD; 1.
 DR Pfam: PF00271; Helicase_C; 1.
 DR SMART: SM00487; DEXDC; 1.
 DR SMART: SM00490; HelicC; 1.
 DR PROSITE: PS00039; DEAD_ATP_HELICASE; 1.
 DR PROSITE: PS00039; Helicase; ATP-binding; RNA-binding;
 KW Hydrolyase; Helicase; ATP-binding; Complete proteome.
 KW Transcription regulation; Complete proteome.
 FT NP_BIND 49 56 ATP (POTENTIAL).
 FT SITE 155 158 DEAD_BOX.
 FT SEQUENCE 613 AA; 69705 MW; 1B826CBDEB1704DF CRC64;

 Query Match 48.1%; Score 50; DB 1; Length 613;
 Best Local Similarity 44.8%; Pred. No. 5.7;

Matches 13; Conservative 3; Mismatches 1; Indels 12; Gaps 2;

QY 3 ENSRG-----KGR-----RQGRGNRG 19
:|||||
Db 556 DNSRGSDDFNGKRGGRGDFRGRGRG 584
:|||||

RESULT 12

VE2_HPV12
ID VE2_HPV12 STANDARD; PRT; 494 AA.

AC P36782;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Regulatory protein E2.
OS E2.

GN Human papillomavirus type 12.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

Papillomavirus.

NCBI_TaxID=10604;

RESULT 13

RP SEQUENCE FROM N.A.
RX MEDLINE=94265501; PubMed=8205838;

RA Delius H., Hofmann B.;

RT "Primer-directed sequencing of human papillomavirus types.";

RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).

CC -!- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.

CC IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACCCNNNGGT-3') PRESENT

CC IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER

CC ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION

CC WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS

CC BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION

CC INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA

CC REPLICATION.

CC -!- SUBUNIT: BINDS DNA AS A DIMER.

CC -!- SUBCELLULAR LOCATION: Nuclear.

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DR EMBL; X74456; CAA52499.1; -

PIR; S36541; S36541.

HSP; P17383; LDHM.

InterPro: IPR000427; E2_C.

DR InterPro: IPR001866; E2_N.

DR Pfam; PF00508; E2_N; 1.

DR Pfam; PF00511; E2_C; 1.

DR ProDom; PD000672; E2_C; 1.

DR ProDom; PD000678; E2_N; 1.

KW Early protein; Transcription regulation; Activator; DNA-binding;

KW Trans-acting factor; DNA replication; Repressor; Nuclear protein.

SQ SEQUENCE 494 AA; 56039 MW; 3C20AF3560C10EE CRC64;

Query Match 47.1%; Score 49; DB 1; Length 494;

Best Local Similarity 69.2%; Pred. No. 6.4;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 RGKGRGRGQGNR 18

II:|||||

Db 344 RGRGRGRGKRR 356

RESULT 13

ROR_HUMAN

ID ROR_HUMAN STANDARD; PRT; 633 AA.

AC O43390;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Heterogeneous nuclear ribonucleoprotein R (hnRNP R).
GN HNRPR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RESULT 14

RP SEQUENCE FROM N.A.

RX MEDLINE=98083170; PubMed=9421497;

RA Hassfeld W., Chan E.K.L., Mathison D.A., Portman D., Dreyfuss G.,

RT Steiner G., Tan E.M.;

RT "Molecular definition of heterogeneous nuclear ribonucleoprotein R

RT (hnRNP R) using autoimmune antibody: immunological relationship with

RT hnRNP P.;"

RL Nucleic Acids Res. 26:439-445(1998).

CC -!- FUNCTION: COMPONENT OF RIBONUCLEOSOMES, WHICH ARE COMPLEXES OF AT

CC LEAST 20 OTHER DIFFERENT HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS

CC (HNRNP). HNRNP PLAY AN IMPORTANT ROLE IN PROCESSING OF PRECURSOR

CC MRNA IN THE NUCLEUS.

CC -!- SUBCELLULAR LOCATION: Nuclear; nucleoplasm.

CC -!- SIMILARITY: CONTAINS 3 RNA RECOGNITION MOTIFS (RRM).

CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; AF000364; AAC39540.1; -

HSP; P09651; 1HA1.

DR Genew; HGNC:5047; HNRPR.

DR InterPro: IPR000504; RNA_rec_mot.

DR Pfam; PF00076; Rrm; 3.

DR SMART; SM00360; RRM; 3.

DR PROSITE; PS00030; RRM_RNP_1; 2.

KW Nuclear protein; RNA-binding; Ribonucleoprotein; Repeat.

FT DOMAIN 1 153 ASP/GLU-RICH (ACIDIC).

FT DOMAIN 412 418 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

FT DOMAIN 165 244 RNA-BINDING (RRM) 1.

FT DOMAIN 246 328 RNA-BINDING (RRM) 2.

FT DOMAIN 341 411 RNA-BINDING (RRM) 3.

FT DOMAIN 447 567 RNA-BINDING (RGX-BOX).

FT DOMAIN 462 497 3 X 11 AA APPROXIMATE REPEATS OF D-D-Y-Y-

FT REPEAT 462 471 G-Y-D-Y-H-D-Y.

FT REPEAT 472 482 1 (APPROXIMATE).

FT REPEAT 488 497 3 (APPROXIMATE).

FT DOMAIN 579 633 GLN/ASN-RICH DOMAIN.

SQ SEQUENCE 633 AA; 70943 MW; 088341F645ED46F CRC64;

Query Match 46.6%; Score 48.5; DB 1; Length 633;

Best Local Similarity 58.8%; Pred. No. 9.6;

Matches 10; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 3 ENSRGKGRGCRGKNGR 19

II:|||||

Db 551 QQGRGRGRGSRG-NRG 566

RESULT 14

YK09_CABEEL

ID YK09_CABEEL STANDARD; PRT; 643 AA.

AC P34304;

DT 01-FEB-1994 (Rel. 28, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Hypothetical protein C06E1.9 in chromosome III.

GN C06E1.9.

OS Caenorhabditis elegans.

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2002, 08:16:37 ; Search time 30 Seconds
(without alignments)
130.497 Million cell updates/sec

Title: US-09-687-993-18

Perfect score: 104

Sequence: 1 NPENSRGKRRGQGRGKNGR 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvivirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	100.0	133	4	Q9UD32
2	104	100.0	185	4	Q96144
3	101	97.1	160	6	O97685
4	99	95.2	73	11	Q9QXJ7
5	99	95.2	99	11	Q9QXJ8
6	99	95.2	125	11	Q9QXJ9
7	99	95.2	199	11	Q8R485
8	72	69.2	182	13	Q9IAM2
9	72	69.2	215	13	Q9IAM3
10	71	68.3	143	13	Q8QGE9
11	60	57.7	926	10	Q9LVP1
12	58	55.8	1479	10	Q9ATY5
13	58	55.8	1522	10	Q9LRT2
14	57	54.8	513	10	Q8RZE5
15	55.5	53.4	545	10	Q8S6K4
16	55.5	53.4	2925	12	O89163

ALIGNMENTS

RESULT 1

Q9UD32 PRELIMINARY; PRT; 133 AA.

ID Q9UD32;

AC Q9UD32; (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE ASTROCYTE-derived TROPHIC factor 2, ATF-2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=95172201; PubMed=7867768;

RA Schaar D.G., Sleber B.A., Sherwood A.C., Dean D., Mendoza G.,

RA Ramakrishnan L., Dreyfus C.F., Black I.B.;

RT *Multiple astrocyte transcripts encode nigral trophic factors in rat

RL and human.;

RL Exp. Neurol. 130:387-393(1994).

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

DR HSSP: Q07731; IAGO.

DR InterPro: IPR001839; TGFb.

DR Pfam: PF00019; TGF-beta; 1.

DR SMART: SM00204; TGFb; 1.

KW Glycoprotein.

SQ SEQUENCE 133 AA; 14736 MW; B46B96DD5F679769 CRC64;

Query Match

Best Local Similarity 100.0%; Score 104; DB 4; Length 133;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPENSRGKRRGQGRGKNGR 19

|||||

Db 21 NPENSRGKRRGQGRGKNGR 39

RESULT 2

Q96144

Q91gn8 rice grassy
Q94749 caulobacter
Q94qu5 oryza sativ
Q94iw2 oryza sativ
Q9vfw2 drosophila
Q91pq8 cynomolgus
Q9nka5 drosophila
Q9c2k5 neospora
Q8ug82 agrobacteri
Q91ok1 arabidopsis
Q9c7yl arabidopsis
Q9fth39 arabidopsis
Q99dc5 human immun
Q99da5 human immun
Q99da0 human immun
Q91136 human immun
Q91140 human immun
Q91144 human immun
Q91152 human immun
Q9ync9 human immun
Q91170 human immun
Q9ync7 human immun
Q9ync6 human immun
Q91180 human immun
Q900y9 human immun
Q99z38 streptococ
Q51287 neisseria m
Q9sfy4 arabidopsis
Q9mau9 arabidopsis

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ID Q96L44 PRELIMINARY; PRT; 185 AA.
AC Q96L44;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE GDNF splice variant 3 (Fragment).
GN GDNF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang B., Peng X., Zhou Y., Peng X., Yuan J., Qiang B.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AY052832; AAL11017.1; -.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF-beta; 1.
KW Glycoprotein.
SQ SEQUENCE 185 AA; 20885 MW; 1988C50DA5EA1B10 CRC64;

Query Match 100.0%; Score 104; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPENSRGKGRGORGKNGR 19
DB 73 NPENSRGKGRGORGKNGR 91

RESULT 3
O97685 PRELIMINARY; PRT; 160 AA.
AC O97685;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Neurotrophic factor (Fragment).
GN GDNF.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Erjia C., Yong L., QiuJiang D.;
RL "The gene cloning of macaca and human GDNF by direct PCR from whole
blood and sequence analysis."
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF106678; AAC99782.1; -.
DR HSSP; Q07731; IAGQ.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF-beta; 1.
DR SMART; SM00204; TGFb; 1.
KW Glycoprotein.
FT NON_TER 1
SQ SEQUENCE 160 AA; 18196 MW; E206362185D499B4 CRC64;

Query Match 97.1%; Score 101; DB 6; Length 160;
Best Local Similarity 94.7%; Pred. No. 5.4e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPENSRGKGRGORGKNGR 19
DB 48 NPENSRGKGRGORGKNGR 66

RESULT 4
O9QXJ7 PRELIMINARY; PRT; 73 AA.
ID Q9QXJ7

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AC Q9QXJ7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GDNF splice variant 3 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Russell F.D., Koishi K., Jiang Y., McLennan I.S.;
RL "Anterograde axonal transport of glial cell line-derived neurotrophic
factor and its receptors in rat hypoglossal nerve."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF205715; AAF23769.1; -.
FT NON_TER 73
SQ SEQUENCE 73 AA; 8262 MW; D6394FE64FFC67AB CRC64;

Query Match 95.2%; Score 99; DB 11; Length 73;
Best Local Similarity 94.7%; Pred. No. 4.7e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPENSRGKGRGORGKNGR 19
DB 47 SPENSRGKGRGORGKNGR 65

RESULT 5
O9QXJ8 PRELIMINARY; PRT; 99 AA.
ID Q9QXJ8
AC Q9QXJ8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GDNF splice variant 2 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Russell F.D., Koishi K., Jiang Y., McLennan I.S.;
RL "Anterograde axonal transport of glial cell line-derived neurotrophic
factor and its receptors in rat hypoglossal nerve."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF205714; AAF23768.1; -.
FT NON_TER 99
SQ SEQUENCE 99 AA; 11025 MW; C60C998CD9C58723 CRC64;

Query Match 95.2%; Score 99; DB 11; Length 99;
Best Local Similarity 94.7%; Pred. No. 6.5e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPENSRGKGRGORGKNGR 19
DB 73 SPENSRGKGRGORGKNGR 91

RESULT 6
O9QXJ9 PRELIMINARY; PRT; 125 AA.
ID Q9QXJ9
AC Q9QXJ9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GDNF splice variant 1 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

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[1]
RN SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=BRAIN;
RA Russell F.D., Koishi K., Jiang Y., McLennan I.S.;
RT "Anterograde axonal transport of glial cell line-derived neurotrophic
factor and its receptors in rat hypoglossal nerve.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF205713; AAF23767.1; -.
KW NON_TER 125
SQ SEQUENCE 125 AA; 13881 MW; 5879E8E5A7190279 CRC64;

Query Match 95.2%; Score 99; DB 11; Length 125;
Best Local Similarity 94.7%; Pred. No. 8.4e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPENSRGKGRRGQGRGNRG 19
Db :|||||
99 SPENSRGKGRRGQGRGNRG 117
Db :|||||

RESULT 7
Q8R485
ID Q8R485 PRELIMINARY; PRT; 199 AA.
AC Q8R485;
DT 01-JUN-2002 (TEMBLrel. 21, Created)
DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Neurotrophic factor GDNF (Fragment).
GN GDNF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21927466; PubMed=11930164;
RA Armstrong K.J., Niles L.P.;
RT "Induction of GDNF mRNA expression by melatonin in rat C6 glioma
cells.";
RL Neuroreport 13:473-475(2002).
DR EMBL; AF497634; AAM18096.1; -.
KW NON_TER 199
FT NON_TER 199
SQ SEQUENCE 199 AA; 22299 MW; 0F3D222869386F7D CRC64;

Query Match 95.2%; Score 99; DB 11; Length 199;
Best Local Similarity 94.7%; Pred. No. 1.4e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPENSRGKGRRGQGRGNRG 19
Db :|||||
91 SPENSRGKGRRGQGRGNRG 109
Db :|||||

RESULT 8
Q9IAM2
ID Q9IAM2 PRELIMINARY; PRT; 182 AA.
AC Q9IAM2;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Glial cell line-derived neurotrophic factor short form
(Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20092738; PubMed=10625540;
RA Homma S., Oppenheim R.W., Yaginuma H., Kimura S.;
RT "Expression pattern of GDNF, c-ret, and GFRalpha3 suggests novel roles
for GDNF ligands during early organogenesis in the chick embryo.";
RL Dev. Biol. 217:121-137(2000).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF176017; AAF26684.1; -.
KW HSP; Q07731; IAGO.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF-beta; 1.
DR SMART; SM00204; TGFb; 1.
KW Glycoprotein.
FT NON_TER 1
FT NON_TER 215
SQ SEQUENCE 215 AA; 24150 MW; 46A45417EADF8DA0 CRC64;

Query Match 69.2%; Score 72; DB 13; Length 215;
Best Local Similarity 73.7%; Pred. No. 0.0022;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 NPENSRGKGRRGQGRGNRG 19
Db :|||||
104 NVENSSKGRNRQGRGNRG 122
Db :|||||

RESULT 10
Q8QGE9
ID Q8QGE9 PRELIMINARY; PRT; 143 AA.
AC Q8QGE9;
DT 01-JUN-2002 (TEMBLrel. 21, Created)
DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Glial cell line-derived neurotrophic factor GDNF (Fragment).
GN GDNF.
OS Nipponia nippon.
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```

RT for GDNF ligands during early organogenesis in the chick embryo.";
RL Dev. Biol. 217:121-137(2000).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF176018; AAF26685.1; -.
DR HSP; Q07731; IAGO.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF-beta; 1.
DR SMART; SM00204; TGFb; 1.
KW Glycoprotein.
FT NON_TER 1
FT NON_TER 182
SQ SEQUENCE 182 AA; 20740 MW; 6ABAC16BD1B4F103 CRC64;

Query Match 69.2%; Score 72; DB 13; Length 182;
Best Local Similarity 73.7%; Pred. No. 0.0018;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 NPENSRGKGRRGQGRGNRG 19
Db :|||||
71 NVENSSKGRNRQGRGNRG 89
Db :|||||

RESULT 9
Q9IAM3
ID Q9IAM3 PRELIMINARY; PRT; 215 AA.
AC Q9IAM3;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Glial cell line-derived neurotrophic factor long form (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20092738; PubMed=10625540;
RA Homma S., Oppenheim R.W., Yaginuma H., Kimura S.;
RT "Expression pattern of GDNF, c-ret, and GFRalpha3 suggests novel roles
for GDNF ligands during early organogenesis in the chick embryo.";
RL Dev. Biol. 217:121-137(2000).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF176017; AAF26684.1; -.
KW HSP; Q07731; IAGO.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF-beta; 1.
DR SMART; SM00204; TGFb; 1.
KW Glycoprotein.
FT NON_TER 1
FT NON_TER 215
SQ SEQUENCE 215 AA; 24150 MW; 46A45417EADF8DA0 CRC64;

Query Match 69.2%; Score 72; DB 13; Length 215;
Best Local Similarity 73.7%; Pred. No. 0.0022;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 NPENSRGKGRRGQGRGNRG 19
Db :|||||
104 NVENSSKGRNRQGRGNRG 122
Db :|||||

RESULT 10
Q8QGE9
ID Q8QGE9 PRELIMINARY; PRT; 143 AA.
AC Q8QGE9;
DT 01-JUN-2002 (TEMBLrel. 21, Created)
DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Glial cell line-derived neurotrophic factor GDNF (Fragment).
GN GDNF.
OS Nipponia nippon.
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
```

OC Archosauaria; Aves; Neognathae; Ciconiiformes; Threskiornithidae;

OC Nipponia.

OX NCBI_TaxID=128390;

RN [1]

RP SEQUENCE FROM N.A.

RA Zheng H., Fang S., Xi Y., Fujihara N.;

RT "Cloning and expression of glial cell line-derived neurotrophic factor

(GDNF) of Nipponia nippon.";

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF469665; AAL79041.1; "

FT NON_TER 1

FT 143

SQ SEQUENCE 143 AA; 16507 MW; 26ADB9C00B6231E CRC64;

Query Match

Best Local Similarity 58.3%; Score 71; DB 13; Length 143;

Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 NPNSRGKGRRGGRGKNGR 19

| | | | | | | | | | | | | | |

31 NIENSSKKGRNRQKNGR 49

RESULT 11

Q9LVP1

ID Q9LVP1 PRELIMINARY; PRT; 926 AA.

AC Q9LVP1;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Arabidopsis thaliana (EC 5.99.1.2).

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

OX [1]

RN SEQUENCE FROM N.A.

RP STRAIN=COLUMBIA;

RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,

RA Tabata S.;

RT Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence

features of the regions of 3,076,755 bp covered by sixty P1 and TAC

clones.";

RL DNA Res. 7:31-63(2000).

CC -!- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE

CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER (BY

SIMILARITY).

-!- CATALYTIC ACTIVITY: ATP-INDEPENDENT BREAKAGE OF SINGLE-STRANDED

DNA, FOLLOWED BY PASSAGE AND REJOINING.

-!- MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA

BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN

WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS

AT ONE END OF THE ENZYME-SEVERED DNA STRAND (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE

FAMILY.

EMBL; AB019227; BAA96895.1; "

InterPro: IPR002936; DNAtprim_toprim.

InterPro: IPR003601; DNAtop_ATP_bind.

InterPro: IPR003602; DNAtop_ATP_bind.

InterPro: IPR000380; Prok_tpisomrase.

DR InterPro: IPR001878; znf_CCHC.

DR Pfam; PF01131; Topoisom_bac; 1.

DR Pfam; PF01751; Toprim; 1.

DR Pfam; PF01396; zf-C4_Topoisom; 1.

DR Pfam; PF00098; zf-CCHC; 2.

DR PRINTS; PR00417; PRTPISMRASEI.

DR SMART; SM00437; TOP1AC; 1.

DR SMART; SM00436; TOP1Bc; 1.

DR SMART; SM00493; TOP1W; 1.

DR SMART; SM00343; znf_C2HC; 2.

DR PROSITE; PS00396; TOPOISOMERASE_I_PROK; 1.

KW DNA-binding; Isomerase; Topoisomerase.

SQ SEQUENCE 926 AA; 103407 MW; 806A59EAD08CBB08 CRC64;

Query Match

Best Local Similarity 57.7%; Score 60; DB 10; Length 926;

Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 NSRGKGRRGGRGKNGR 19

| | | | | | | | | | | | | | |

DB 857 NSGSGRGRGSRGRGRG 872

RESULT 12

Q9ATY5

ID Q9ATY5 PRELIMINARY; PRT; 1479 AA.

AC Q9ATY5;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE UV hypersensitive protein.

GN UVH3

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

OX [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21332854; PubMed=11439121;

RA Liu Z., Hail J.D., Mount D.W.;

RT "Arabidopsis UVH3 gene is a homolog of the Saccharomyces cerevisiae

RAD2 and human XPG DNA repair genes.";

RL Plant J. 26:329-338(2001).

DR EMBL; AF312711; AAK37472.1; "-

DR InterPro: IPR000513; Exo_N_I.

DR InterPro: IPR003584; HHH_2.

DR InterPro: IPR001532; XPGC_Rad.

DR Pfam; PF00867; XPG_I; 1.

DR Pfam; PF00752; XPG_N; 1.

DR PRINTS; PR00853; XPGRADSUPER.

DR SMART; SM00279; HHG2; 1.

DR SMART; SM00484; XPGI; 1.

DR SMART; SM00485; XPGN; 1.

DR PROSITE; PS00842; XPG_2; 1.

SQ SEQUENCE 1479 AA; 165666 MW; 72F38D472849EE55 CRC64;

Query Match

Best Local Similarity 55.8%; Score 58; DB 10; Length 1479;

Matches 10; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 PENSRGKGRRGGRGKNGR 19

| | | | | | | | | | | | | | |

DB 1264 PSSRGRGRGKNGRGRG 1281

RESULT 13

Q9LRT2

ID Q9LRT2 PRELIMINARY; PRT; 1522 AA.

AC Q9LRT2;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Similarity to nucleotide excision repair protein.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

OX [1]

RP SEQUENCE FROM N.A.

RC STRAIN=COLUMBIA;

RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

```

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20363099; PubMed=10907853;
RA Nakamura Y.;
RT *Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,
RT TAC and BAC clones.*;
RL DNA Res. 7:217-221(2000).
DR EMBL: AB028616; BAB01125.1; -.
DR InterPro: IPR000513; EXO_N.I.
DR InterPro: IPR003584; HHR_2.
DR InterPro: IPR001532; XPGC_Rad.
DR Pfam: PF00867; XPG_I; 1.
DR Pfam: PF00752; XPG_N; 1.
DR PRINTS: PR00853; XPGRADSUPER.
DR SMART: SM00279; HHR2; 1.
DR SMART: SM00484; XPGI; 1.
DR SMART: SM00485; XPGN; 1.
DR PROSITE: PS00842; XPG_2; 1.
SEQUENCE 1522 AA; 170399 MW; D189F84F4C76CB45 CRC64;

Query Match 55.8%; Score 58; DB 10; Length 1522;
Best Local Similarity 55.6%; Pred. No. 2.5;
Matches 10; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 PENSRGKRRGQGRGKNRG 19
DB 1304 PSSSRGGRGAQKRGGRG 1321

RESULT 14
Q8RZE5 PRELIMINARY; PRT; 513 AA.
AC Q8RZE5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative AAA-type ATPase-like protein.
GN P0510C12.7.
OS Oryza sativa (japonica cultivar-group). Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RX Sasaki T., Matsumoto T., Yamamoto K.;
RT *Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0510C12.*;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF003725; BAB90463.1; -.
SQ SEQUENCE 513 AA; 55589 MW; 05CDDBE17327314A CRC64;

Query Match 54.8%; Score 57; DB 10; Length 513;
Best Local Similarity 64.7%; Pred. No. 1.1;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 ENSRGKRRGQGRGKNRG 19
DB 495 E1SHGQGRGVRGVRGGRG 511

RESULT 15
Q8S6K4 PRELIMINARY; PRT; 545 AA.
AC Q8S6K4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 62.7 kDa protein.
GN OSJNBA0019N10.22.

```

```

OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIPPONBARE;
RX McCombie W.R., de la Bastide M., Spiegel L., Preston R., Kirchoff K.,
RA Kuit K., Nascimento L., Zutavern T., Balija V., Bell M., Baker J.,
RA Santos L., Miller B., Katzenberger F., Muller S., King L., Yang C.,
RA O'Shaughnessy A., Palmer L., Dedhia N.;
RT *Genomic sequence for Oryza sativa, Nipponbare strain, clone
RT OSJNBA0019N10, from chromosome 10, complete sequence.*;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC092748; RAM01084.1; -.
KW Hypothetical protein.
SQ SEQUENCE 545 AA; 62654 MW; 799E292BE497DC90 CRC64;

Query Match 53.4%; Score 55.5; DB 10; Length 545;
Best Local Similarity 50.0%; Pred. No. 2;
Matches 14; Conservative 2; Mismatches 3; Indels 9; Gaps 2;

QY 1 NPEN-----SRGKRRGQ-RGKNRG 19
DB 482 NPANFEKVRKAMSGRGRGRPRGSRG 509

Search completed: December 4, 2002, 08:18:53
Job time : 32 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2002, 08:18:02 ; Search time 15 Seconds
(without alignments)
37.269 Million cell updates/sec

Title: US-09-687-993-18
Perfect score: 104
Sequence: 1 NPENSRGKRRGQGRGKNG 19
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Archived: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2.6/ptodata/1/1aa/5A_COMB.pep.*
2: /cgn2.6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2.6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2.6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2.6/ptodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2.6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	104	100.0	19	4 US-08-535-681-18	Sequence 18, Appl
2	104	100.0	20	4 US-08-535-681-19	Sequence 19, Appl
3	104	100.0	21	4 US-08-535-681-20	Sequence 20, Appl
4	104	100.0	22	4 US-08-535-681-21	Sequence 21, Appl
5	104	100.0	23	4 US-08-535-681-22	Sequence 22, Appl
6	104	100.0	24	4 US-08-535-681-23	Sequence 23, Appl
7	104	100.0	25	4 US-08-535-681-24	Sequence 24, Appl
8	104	100.0	26	4 US-08-535-681-25	Sequence 25, Appl
9	104	100.0	27	4 US-08-535-681-26	Sequence 26, Appl
10	104	100.0	28	4 US-08-535-681-27	Sequence 27, Appl
11	104	100.0	29	4 US-08-535-681-28	Sequence 28, Appl
12	104	100.0	30	4 US-08-535-681-29	Sequence 29, Appl
13	104	100.0	31	4 US-08-535-681-30	Sequence 30, Appl
14	104	100.0	32	4 US-08-535-681-31	Sequence 31, Appl
15	104	100.0	33	4 US-08-535-681-32	Sequence 32, Appl
16	104	100.0	34	4 US-08-535-681-33	Sequence 33, Appl
17	104	100.0	35	4 US-08-535-681-34	Sequence 34, Appl
18	104	100.0	36	4 US-08-535-681-35	Sequence 35, Appl
19	104	100.0	37	4 US-08-535-681-36	Sequence 36, Appl
20	104	100.0	38	4 US-08-535-681-37	Sequence 37, Appl
21	104	100.0	39	4 US-08-535-681-38	Sequence 38, Appl
22	104	100.0	134	1 US-08-535-681-1	Sequence 1, Appl
23	104	100.0	134	1 US-08-564-833-1	Sequence 1, Appl
24	104	100.0	134	1 US-08-535-682-1	Sequence 1, Appl
25	104	100.0	134	1 US-08-446-383A-1	Sequence 1, Appl
26	104	100.0	134	1 US-08-795-628-1	Sequence 1, Appl
27	104	100.0	134	1 US-08-519-777-76	Sequence 76, Appl

28	104	100.0	134	1 US-08-618-543-1	Sequence 1, Appl
29	104	100.0	134	1 US-08-742-035-76	Sequence 76, Appl
30	104	100.0	134	1 US-08-777-019-76	Sequence 76, Appl
31	104	100.0	134	2 US-08-606-176A-1	Sequence 1, Appl
32	104	100.0	134	2 US-08-777-143-76	Sequence 76, Appl
33	104	100.0	134	2 US-08-710-219A-1	Sequence 1, Appl
34	104	100.0	134	2 US-08-452-242-6	Sequence 6, Appl
35	104	100.0	134	3 US-08-453-176A-6	Sequence 6, Appl
36	104	100.0	134	3 US-08-775-414-76	Sequence 76, Appl
37	104	100.0	134	3 US-08-451-374-6	Sequence 6, Appl
38	104	100.0	134	4 US-08-535-681-2	Sequence 2, Appl
39	104	100.0	134	4 US-08-935-268A-6	Sequence 6, Appl
40	104	100.0	134	4 US-08-931-858E-76	Sequence 76, Appl
41	104	100.0	134	4 US-08-981-739-76	Sequence 76, Appl
42	104	100.0	134	4 US-09-220-528-13	Sequence 13, Appl
43	104	100.0	134	4 US-08-452-229-6	Sequence 6, Appl
44	104	100.0	134	4 US-09-128-026-76	Sequence 76, Appl
45	104	100.0	135	4 US-08-535-681-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-08-535-681-18
; Sequence 18, Application US/08535681
; Patent No. 6184200
; GENERAL INFORMATION:
; APPLICANT: Hu, Sylvia
; TITLE OF INVENTION: Truncated Glial Cell Line-Derived Neurotrophic
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,681
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Curry, Daniel R.
; REGISTRATION NUMBER: 32,727
; REFERENCE/DOCKET NUMBER: A-357
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805-447-8102
; TELEFAX: 805-499-8011
; TELEX:
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-535-681-18

Query Match 100.0%; Score 104; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.9e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NPENSRGKRRGQGRGKNG 19
|||||
Db 1 NPENSRGKRRGQGRGKNG 19

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RESULT 2
US-08-535-681-19
; Sequence 19, Application US/08535681
; Patent No. 6184200
; GENERAL INFORMATION:
; APPLICANT: Hu, Sylvia
; TITLE OF INVENTION: Truncated Glial Cell Line-Derived Neurotrophic
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,681
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Curry, Daniel R.
; REGISTRATION NUMBER: 32,727
; REFERENCE/DOCKET NUMBER: A-357
; TELEPHONE: 805-447-8102
; TELEFAX: 805-499-8011
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-535-681-19
Query Match 100.0%; Score 104; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPNSRGKRRGGRGKNG 19
DB 2 NPNSRGKRRGGRGKNG 20
; GENERAL INFORMATION:
; APPLICANT: Hu, Sylvia
; TITLE OF INVENTION: Truncated Glial Cell Line-Derived Neurotrophic
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,681
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Curry, Daniel R.
; REGISTRATION NUMBER: 32,727
; REFERENCE/DOCKET NUMBER: A-357
; TELEPHONE: 805-447-8102
; TELEFAX: 805-499-8011
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-535-681-19
Query Match 100.0%; Score 104; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPNSRGKRRGGRGKNG 19
DB 2 NPNSRGKRRGGRGKNG 20
; GENERAL INFORMATION:
; APPLICANT: Hu, Sylvia
; TITLE OF INVENTION: Truncated Glial Cell Line-Derived Neurotrophic
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,681
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Curry, Daniel R.
; REGISTRATION NUMBER: 32,727
; REFERENCE/DOCKET NUMBER: A-357
; TELEPHONE: 805-447-8102
; TELEFAX: 805-499-8011
; TELEX:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-535-681-21
Query Match 100.0%; Score 104; DB 4; Length 22;
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,681
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Curry, Daniel R.
; REGISTRATION NUMBER: 32,727
; REFERENCE/DOCKET NUMBER: A-357
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805-447-8102
; TELEFAX: 805-499-8011
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-535-681-20
Query Match 100.0%; Score 104; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPNSRGKRRGGRGKNG 19
DB 3 NPNSRGKRRGGRGKNG 21
; GENERAL INFORMATION:
; APPLICANT: Hu, Sylvia
; TITLE OF INVENTION: Truncated Glial Cell Line-Derived Neurotrophic
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,681
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Curry, Daniel R.
; REGISTRATION NUMBER: 32,727
; REFERENCE/DOCKET NUMBER: A-357
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805-447-8102
; TELEFAX: 805-499-8011
; TELEX:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-535-681-21
Query Match 100.0%; Score 104; DB 4; Length 22;
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-535-681-24

Query Match 100.0%; Score 104; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPENSRGKRRGGRGKNG 19
|||||
Db 7 NPENSRGKRRGGRGKNG 25

RESULT 8

US-08-535-681-25
Sequence 25, Application US/08535681
Patent No. 6184200
GENERAL INFORMATION:

APPLICANT: Hu, Sylvia
TITLE OF INVENTION: Truncated Glial Cell Line-Derived Neurotrophic

NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.

STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: United States of America
ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/535,681
FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Curry, Daniel R.
REGISTRATION NUMBER: 32,727
REFERENCE/DOCKET NUMBER: A-357

TELECOMMUNICATION INFORMATION:

TELEPHONE: 805-447-8102
TELEFAX: 805-499-8011

TELEX:

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-535-681-25

Query Match 100.0%; Score 104; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.2e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPENSRGKRRGGRGKNG 19
|||||
Db 8 NPENSRGKRRGGRGKNG 26

RESULT 9

US-08-535-681-26

Sequence 26, Application US/08535681
Patent No. 6184200
GENERAL INFORMATION:

APPLICANT: Hu, Sylvia

TITLE OF INVENTION: Truncated Glial Cell Line-Derived Neurotrophic

TITLE OF INVENTION: Factor
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: United States of America
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/535,681

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Curry, Daniel R.

REGISTRATION NUMBER: 32,727

REFERENCE/DOCKET NUMBER: A-357

TELECOMMUNICATION INFORMATION:

TELEPHONE: 805-447-8102

TELEFAX: 805-499-8011

TELEX:

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-535-681-26

Query Match 100.0%; Score 104; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPENSRGKRRGGRGKNG 19
|||||

Db 9 NPENSRGKRRGGRGKNG 27

RESULT 10

US-08-535-681-27

Sequence 27, Application US/08535681
Patent No. 6184200
GENERAL INFORMATION:

APPLICANT: Hu, Sylvia

TITLE OF INVENTION: Truncated Glial Cell Line-Derived Neurotrophic

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: AMGEN INC.

STREET: 1840 DeHavilland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: United States of America

ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/535,681

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Curry, Daniel R.

REGISTRATION NUMBER: 32,727

REFERENCE/DOCKET NUMBER: A-357

TELECOMMUNICATION INFORMATION:
TELEPHONE: 805-447-8102
TELEFAX: 805-499-8011
TELEX:
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-535-681-27

Query Match 100.0%; Score 104; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.6e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 NPENSRGKGRGGRGKNG 19
|||||
10 NPENSRGKGRGGRGKNG 28

RESULT 11
US-08-535-681-28
Sequence 28, Application US/08535681
Patent No. 6184200
GENERAL INFORMATION:
APPLICANT: Hu, Sylvia
TITLE OF INVENTION: Truncated Glial Cell Line-Derived Neurotrophic
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: United States of America
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,681
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Curry, Daniel R.
REGISTRATION NUMBER: 32,727
REFERENCE/DOCKET NUMBER: A-357
TELEPHONE: 805-447-8102
TELEFAX: 805-499-8011
TELEX:
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-535-681-28

Query Match 100.0%; Score 104; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.8e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 NPENSRGKGRGGRGKNG 19
|||||
11 NPENSRGKGRGGRGKNG 29

RESULT 12
US-08-535-681-29
Sequence 29, Application US/08535681
Patent No. 6184200
GENERAL INFORMATION:
APPLICANT: Hu, Sylvia
TITLE OF INVENTION: Truncated Glial Cell Line-Derived Neurotrophic
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: United States of America
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,681
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Curry, Daniel R.
REGISTRATION NUMBER: 32,727
REFERENCE/DOCKET NUMBER: A-357
TELEPHONE: 805-447-8102
TELEFAX: 805-499-8011
TELEX:
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-535-681-29

Query Match 100.0%; Score 104; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 6e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPENSRGKGRGGRGKNG 19
|||||
Db 12 NPENSRGKGRGGRGKNG 30

RESULT 13
US-08-535-681-30
Sequence 30, Application US/08535681
Patent No. 6184200
GENERAL INFORMATION:
APPLICANT: Hu, Sylvia
TITLE OF INVENTION: Truncated Glial Cell Line-Derived Neurotrophic
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: United States of America
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

Query Match 100.0%; Score 104; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 6.4e-09;